U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

Requestor's		Serial Numbe	»r•		
	Phone:	Numbe		t:	
terms that may have a speci	ment of search topic. Descri al meaning. Give examples sequence. You may include :	or relevent citations, aut	hors, keywords, etc	., 11 known. Por seq	efine any uences,
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Schreider, David

From:

Yu, Misook

Sent:

Wednesday, August 14, 2002 12:56 PM

To: Subject: Schreiber, David

09/499,662

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"M Seruh notes

David,

Is it possible search

1. (X, 18-30 aa)-SEQ ID NO:2-(X, 14 aa)-SEQ ID NO:3-(X, 32 aa)-SEQ ID NO:4-(X, 11 aa) string and

2. (X, 23aa)-SEQ ID NO:5-(X, 15 aa)-SEQ ID NO:6-(X, 32 aa)-SEQ ID NO:7-(X, 10 aa)?

All the SEQ ID NO are small peptides.

Please compare SEQ ID NO:50, 52, 54, 109, 107, 129, 131, 127 against each other. I would like to know what is the differenenes in the seqs. They are all 218 aa antibody light chain.

Please compare SEQ ID NO:89, 117, 143, 145, 147, 155 against each other.

Please search SEQ ID 129, 131, 127, 143, 145, 147, 157. They are all amino acid sequences either 218 or 451 aa.

Please search SEQ ID NO:1 (10aa)

Do I have to get approval from someone for these many seq searches?

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

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GenCore version 4.5
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August 14, 2002, 15:23:12; Search time 53.64 Seconds (without alignments) 7.218 Million cell updates/sec Run on:

US-09-499-662-1 59 1 RTQNTKCRCK 10 Title: Perfect score: Sequence: BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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50	100.		Н	TNR6_HUMAN	homo	sapien
55	93.2	323	Н	TNR6_BOVIN	bos t	taurus
51	86.	327	Н	TNR6_MOUSE	snu	musculu
40	. 79	468	Н	T10A_HUMAN	homo	sapien
39	. 99	272	П	TNR4_MOUSE	mus	musculu
33	1.99	277	-	TNR4_HUMAN	homod	sapien
37	62.	360	7	WNT2_MOUSE	mus m	musculu
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36	61.	58	٦	SCK2_MESMA	Q9nii5 mesobuthus	thus
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36	61.	310	Н	YAHB_ECOLI		ichia
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36	61.	351	٦	WN2B_XENLA	P87387 xenopus lae	s lae
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35	59.	440	-	T10B_HUMAN	homo	sapien
35	59.	842	П	ORP7_HUMAN	homo	sapien
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34	57.	98	Т	TAT_HV1ND	P18804 human	immun
34	57.	66	-	TAT_HV1EL	_	immun
34	57.	148	Н	VEGH_ORFN7	P52585 orf virus	rus (
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SRP_DROME ORN3_PLAOR ORN3_PLAOR ORN3_PLAOR ORN3_PLAOR SCX1_MESMA MT2_CALSI SZ13_MOUSE TAT_HV2SB CR2_HORVU IL2A_CANFA COAT_RCIMV MUB1_XENLA	ALIGNMENTS PRT; 324	50	ta; Craniata; V ia; Sciurognath	SUE=Liver; 507668; katsuki T.; coding a trunca	A CYTOKINE LIG A CYTOKINE LIG RECRUITS CASPAS S AGGREGATE CAL S PERFORMS CAS	PASE-8 INITIALE ECIFIC CYSTEINE D APOPTOSIS MAY L TOLERANCE, IN LLS, OR BOTH (B IYPE I MEMDIANE TH DOMAIN INVOL	OSOLIC ADAPTOR TNFR-CYS REPEA DEATH DOMAIN.	opyright. It is te of Bioinform s Institute. T tutions as long t is not remove a agreement (Se edisp-sib.ch).	
57.6 55.9 55.9 55.9 55.9 55.9 55.9 55.9 55	STANDARD;	99 (Rel. 38, Created) 99 (Rel. 38, Last seq 01 (Rel. 40, Last ann rosis factor receptor (Apoptosis-mediating	rl OR FAS. jicus (Rat). stazoa; Chordata; theria; Rodentia;	M N.A. JE-DAWLEY; TISS 3114; PubMed=73 amamoto M., Wal	phys. Res. Commonly Receptor FOR WOLECULE FADD TO THE RESULTING TO COMPLEX (DISK) A ACHIVE PAGE TO THE RESULT OF T	JN. ACIIVE CAS, (ASPARTATE-SPI S. FAS-MEDIATE S. OF PERIPHERA, DF MATURE T-CE LAR LOCATION:	TO OTHER CYTORY: CONTAINS 3	Nor entry is construction bioinformatic profit institutes the statement in statement in statement in some some some some some some some some	BAA05108.1; 1DDF. (2000488; Death. 7000488; Death. 11; TNFR_C6; 3.05; TNFR_C6; 3.05; TNFR; 3.18; TNFR; 3.0652; TNFR_NGFR_0050; TNFR_NGFR_0050;
######################################	JLT 1 5_RAT TNR6_RAT	063199; 15-JUL-1999 (Rel. 38, 15-JUL-1999 (Rel. 38, 16-CCT-2001 (Rel. 40, Tumor necrosis factor receptor) (Apoptosis-m	(CD95). TNFRSFG OR PT1 OR F Rattus norvegicus (Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;	SEQUENCE FROI STRAIN-SPRAGG MEDLINE-94126 Kimura K., Ye	Lie fat livel Biochem. Biol -!- FUNCTION ADAPTOR N RECEPTOR SIGNALING	CASPASES CASPASES APOPTOSIS INDUCTION SUICIDE (-!- SUBCELLUI)	AND MAYBI	This SWISS-Plactween the the European use by non-modified and entities requor send an en	EMBL; D26112; BAA05108.1; HSSP; P25445; 1DDF. InterPro; 1PR000488; Death. InterPro; 1PR001368; THFR_C6 Pfam; PF000531; death; 1. Pfam; PF00020; TNFR_C6; 3. SMART; SM00005; DARTH; 1. PROSITE; PS00652; TNFR, 3. PROSITE; PS00652; TNFR, NGFR
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InterPro; IPR000488; Death.
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Tar Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

LIENTION: RECEPTOR FOR A CYTOKINE LICAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CRICALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC
ACTIVATION. RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTECASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERLIPHERAL TOLERANCE, IN THE BANTICHN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

LISUBGELLULAR LOCATION: Type I membrane protein.

LOWARIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CHARLING CONTAINS 3 THRR-CYS REPEARS.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
            Transmembrane; Repeat; Signal.
                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                       BY SIMILARITY.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                    100.0%; Score 59; DB 1; Length 324; 100.0%; Pred. No. 0.0013; Ive 0; Mismatches 0; Indels
                                                          EXTRACELLULAR (POTENTIAL).
                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                               SUPERFAMILY MEMBER 6.
                                                                                                                                                                                                                                                                                                                                                          332 AA.
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TNFR-CYS 2.
TNFR-CYS 3.
        Glycoprotein;
21 RY STM
PS50017; DEATH_DOMAIN; 1.
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Best Local Similarity 100.
Matches 10; Conservative
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            Receptor;
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           Apoptosis;
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077736;
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Gaps
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 41, Last annotation update)
1-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDING=1713127;
MEDINE=91309137; PubMed=1713127;
Sameshima M., Hase A., Seto Y., Nagata S.;
"The polypeptide encoded by the CDNA for human cell surface antigen Fas can mediate apoptosis.";
Cell 66:233-243(1991).
         Pfam: PF0053; death; 1.
Pfam: PF0053; death; 1.
Pfam: PF0052; TNFR_c6; 3.
SWART; SW0005; DEATH; 1.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 1 332 TUMON NECROSIS FACTOR RECEPTOR
CHAIN 17 332 TUMON NECROSIS FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335 MEDLINE-92268122; Pubmed-1375228;
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N-LINKED (GLCNAC. .) (POTENTIAL).
5B8B03682756BF1B CRC64;
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Li Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
Krammer P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and molecular cloning of the APO-1 cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59; DB 1; Length 332; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
DEATH.
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IPR001368; TNFR_c6.
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TISSUE=Urinary bladder;
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  InterPro;
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                                                                                                          THE CONTINUE RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE REGULING AGREEATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC OFFICIAL OFFICIA
                                          Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.; "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain."; Nature 384:638-641(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00006; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00050; TNFR_NGFR_1; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
APOPTOSIS; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
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STRUCTURE BY NMR OF 218-335.
MEDLINE-97122332; Pubmed-8967952;
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190
335
83
127
1166
314
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MIM; 134637; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
136
335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
174
191
47
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84
128
230
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SIGNAL
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TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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Score 55; DB 1; Length 323;
Pred. No. 0.0065;
1; Mismatches 0; Indels
                                  1; Mismatches
         93.2%;
                                 Conservative
Query Match
Best Local Similarity
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Gaps

; 0

100.0%; Score 59; DB 1; Length 335; 100.0%; Pred. No. 0.0013; Live 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 10; Conservative

RESULT

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PROSITE; PS50000; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal. ó TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL). 4D88A90E9E1F4892 CRC64; POTENTIAL.
CYTOPLASMIC (POTENTIAL) 323 AA. TNFR-CYS 1. TNFR-CYS 2. TNFR-CYS 3 POTENTIAL. InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
SMART; SM00005; TNFR_c6; 3.
SMART; SM00005; DEATH; 1. 36445 MW; EMBL; U34794; AAC48546.1; -. INFRSF6 OR APT1 OR FAS. Bovidae; Bovinae; Bos. Bos taurus (Bovine). HSSP; P25445; 1DDF. 323 AA; SEQUENCE FROM N.A. NCBI_TaxID=9913; 171 171 189 45 81 125 238 INR6_BOVIN DOMAIN TRANSMEM DOMAIN REPEAT DOMAIN SEQUENCE SIGNAL P51867 REPEAT REPEAT CHAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
LIVER, LUNG, HEARY, AND ADULT OVARY.
-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
-!- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAPTOR WOLKELE FADD RECKUITS CASPAGE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERPORAS CASPAGE-8 PORTOEDLYITC ACTIVATION. ACTIVE CASPAGE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING ACTIVATION OF PERPORAS MAY HAVE A ROLE IN THE INDUCTION OF PERPHERAL TOLERANCE, IN THE ANTIGEN STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-Wmor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-92148151; PubMed-1371136;
Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
Copeland N.G., Jenkins N.A., Nagata S.;
"The CDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.";
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Lymphoprollferation disorder in mice explained by defects in Fas antigen that mediates apoptosis.";
Nature 356:314-317(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-96 FROM N.A.
MEDLINE-93189576; PubMed-7680478;
Adachi M., Watanabe-Fukunaga R., Nagata S.;
"Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92195401; PubMed-1372394;
Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993)
                                                                                                   327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 3 THFR-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 148:1274-1279(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M83649; AAA37593.1; -.
                                                                                                    STANDARD;
                                                                                                                                                                                                             (CD99):
INFRSF6 OR APTI OR FAS.
                                                                                                                                                                                                                                    (Mouse).
                118 RTRNTKCRCK 127
1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRODUCTION
                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT LPR
                                                                                                   TNR6_MOUSE
P25446;
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                                                                       RESULT 5
TNR6_MOUSE
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 10A precursor (Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL receptor-1) (TRAIL-R1).
TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.; "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).

--- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates apoptosis in a caspase-dependent manner. Can trigger the nuclear
                                                                                                                                                                                                                                                                                                                          Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 1; Length 327;
Pred. No. 0.033;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> N (IN LPR).
F6BFFC5ACE356EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The receptor for the cytotoxic ligand TRAIL."; Science 276:111-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CYS 3.
                                                                                                                                                                       Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 3.
SNART; SN00005; DEATH; 1.
SMART; SN00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEATH
EMBL; S56486; AAB25700.1; JOINED. PTR; A46484; A46544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98090092; PubMed-943027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97238921; PubMed=9082980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                           MGD; MGI:95484; Tnfrsf6.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
37418 1
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  21
327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 TONTKCKCK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                             Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T10A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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T10A_HUMAN
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us-09-499-662-1.rsp

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INFRSF4 OR TXGP1 OR OX40.
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CARBOHYD
CONFLICT
SEQUENCE
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TRANSMEM
DOMAIN
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SIGNAL
CHAIN
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REPEAT
REPEAT
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    qq
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
factor kappaB-pathway and can bind the cytoplasmic adapter molecule FADD/WORTI which engages initiator caspases such as caspase 8 leading to subsequent activation of effector caspases that execute apoptotic death of the cell.
SUBUNIT: can interact with TRADD and RIP.
SUBCELLULAR LOCARION: Type I membrane protein.
TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.
                                                                                                                                                                                                                                                                                                                 PROSITE; PS5001; DENTH-DOMAIN; 1.
PROSITE; PS50052; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; Apoptosis; Glycoptoteln; Transmembrane; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE85DCDC2C8760F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.8%; Score 40; DB 1; Length 468;
66.7%; Pred. No. 3.9;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
DEATH.
                                                                                                                                                                                                                                                                                                                                                                                     SUPERFAMILY MEMBER 10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
                                                                                                       SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50025 MW;
                                                                                                                                                                                                                                                     InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_C6.
                                                                                                                                                                                                                         EMBL; U90875; AAC51226.1; -.
                                                                                                                                                                                                                                                                          Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor) (OX40 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
190
207
211
156
4 68 AA;
                                                                                                                                                                                                                                    P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| |:||
183 TRNTACOCK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TQNTKCRCK 10
                                                                                                                                                                                                                                    HSSP; P19438
MIM; 603611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNR4_MOUSE
P47741;
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
REPEAT
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                                                                                                                                   STRAIN=BALB/C;
MEDLINE=94044756; PubMed=8228223;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.,
"Cloning of mouse Ox40: a T cell activation marker that may mediate
                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein."
                      Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
A -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0065; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 272;
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TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Immunol. 25:926-930(1995).
-i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-95255413; PubMed-7737295;
                                                                                                                                                                                                                                                           T-B cell interactions.";
J. Immunol. 151:5261-5271(1993).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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272 AA;
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Matches 6; Conserv
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                                                                                                                  SEQUENCE FROM N.A.
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                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                           Barclay A.N.;
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ID TNR4_HUMAN
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102 TODIVCRCR 110

2 TONTKCRCK 10

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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95219871; PubMed=7704935;
Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
"Identification of OX40 ligand and preliminary characterization of
P43489; Q13663; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).
                                                                                                                                                                                                                                 MEDLINE-94170844; PubMed-7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Ponatsch C., Stein H.;
"The human OX40 homolog: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 2.

TNFR-CYS 3 (INCOMPLETE).

TNFR-CYS 4.

N-LINKED (GICNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                its activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).
-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TWRR-CYS REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD134 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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EMBL; S76792; AAB33944.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00652; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
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                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P25942; 1CDF. MIM; 600315; -.
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215
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=9606;
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TRANSMEM
DOMAIN
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MEDLINE-91122634; PubMed-2279700;
MEDLINE-91122634; PubMed-2279700;
Gavin B.J., McMahon J.A., McMahon A.P.;
"Expression of multiple novel Wnt-1/int-1-related genes during fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and adult mouse development.";
Genes Dev. 4:2319-2332(1990).
-!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY
SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-201265940; PubMed-2693041;

MCMAIDON J.A., MCMAHON A.P.;

"Nucleotide sequence, chromosomal localization and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL). SEC265FD3815EF1D CRC64;
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                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
WNT-2 protein precursor (IRP protein) (INT-1 related protein).
WNT-2 OR INR-2 OR INR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.7%; Score 37; DB 1; Length 360; 66.7%; Pred. No. 10; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the mouse int-1-related gene.";
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Developmental protein; Glycoprotein; Signal.
1 25 POTENTIAL.
CHAIN 26 360 WNT-2 PROTEIN.
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                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 107:643-650(1989).
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40496 MW;
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                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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319 TRMTKCECK 327
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                                                   WNT2_MOUSE
P21552;
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Gaps

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Score 39; DB 1; Length 277; Pred. No. 3.7; 2; Mismatches 1; Indels

66.1%; illarity 66.7%; Conservative

Query Match Best Local Similarity Matches 6; Conserv us-09-499-662-1.rsp

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MEDLINE-93156721; PubMed-8381516;

A Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;

A Rothe J., Bluethmann H., Gentz R.,

"Genomic organization and promoter function of the murine tumor

"Gentz receptor beta gene.";

MOLECOSIS factor receptor beta gene.";

MOLECOSIS factor receptor FOR TWF-ALPHA. THE ADAPTOR MOLECULE FADD

RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING

AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)

PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE

SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE

PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-I- SUBUNIT THE BINDING TO THE EXTRACELLIAR DOMAINS

PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FRADD. THE RECRUITED TO

THERE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THE SCRUITED TO

THERE CANNATURE AT LEAST THAN DISTINCT SIGNALING CASCADES, APOPTOSIS AND

MILLERS AND AND SIGNAL AND DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Spleen;
MEDLINE=92039815; PubMed=1657766;
MEDLINE=92039815; PubMed=1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Inf receptor type b.";
Immunogenetics 34:338-340(1991).
                      umor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1)
                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.;
Cloning, expression and cross-linking analysis of the murine p55
tumor necrosis factor receptor.";
Eur. J. Immunol. 21:1649-1656(1991).
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBL_raxID=10090;
                                                                                                                                                                                                                               Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94245292; PubMed-8188324;
Bebo B.F., Linthicum D.S.;
"Nucleotide sequence of the TNF type I receptor from a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-KAPPA B SIGNALING (BY SIMILARITY).

-! SUBCELLULAR LOCATION; Type I membrane protein.

-! SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

-! SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91285014; PubMed=1647956;
                                                                                                                                                                                                                  MEDLINE=91187885; PubMed=1849278;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91246168; Pubmed-1645445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endothelioma cell line.";
Immunogenetics 39:450-451(1994).
                                                              INFRSF1A OR INFR1 OR INFR-1.
                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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the Swiss Institute of Bioinformatics and the EMBL outstation
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BY SIMIRED (GICNAC. . .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Repeat; Signal; Apoptosis.
POTENTIAL.
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-SMASE ACTIVATION DOMAIN (NSD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 454;
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0710C2E8C3C2B6D9 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                 EMBL; M60468; AAA39751.1; -.
EMBL; X5928; CAA41922.1; -.
EMBL; X57796; CAA41922.1; -.
EMBL; X57796; CAA40936.1; -.
EMBL; L26349; AAA5936.1; -.
EMBL; M76656; AAA40465.1; -.
EMBL; M76656; AAA40465.1; JOINED.
PIR; A38634; GQMST1.
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                                                                                                                                                                                            PIR, S16677, S16677.
PIR, S19021, S19021.
RISP, P19438, 1EXT.
MGD; MGI:1314884; Tnfrsfla.
InterPro; IPR001488; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00521; death; 1.
ProDom; PF00020; TNFR_C6; 4.
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                                                                                                                                                                                                                                                                                               ProDom; PD000771; TNFR_SMART; SM00005; DEATH; SMART; SMO208; TNFR; 3
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454 AA;
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Matches 6; Conserv
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REPEAT
DOMAIN
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SCK2_MESMA
ID SCK2_MI
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Matches
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                                                                                                                                                                                                                                                                                                                                                                             Fourtier T., Lebrun B., Martin-Eauclaire M.-F., Ishiguro M., Esocubas P., Wu F.Q., Hisada M., Pongs O., Nakajima T.; Purication, characterization, and synthesis of three novel toxins from the Chinese scorpion Buthus martensi, which act on K+ channels."; Blochemistry 36:13473-13482(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM CHANNEL INHIBITORS SUBFAMILY.
                                                                                                                                                          MEDIINE-20164067; PubMed-10698710;
Dai L., Wu J.J., Gu Y.H., Lan Z.D., Ling M.-H., Chi C.-W.;
"Genomic organization of three novel toxins from the scorpion Buthus martensi Karsch that are active on potassium channels.";
Biochem. J. 346:805-809(2000).
                          01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Toxin BmTX2 precursor (Neurotoxin TX2).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20436245; PubMed=10978761;
Zeng X.-C., Zhu Z.H., Li W.-X., Zhu S.-Y., Peng F., Mao X., Liu H.;
Molecular cloning and genomic organization of a K(+) channel toxin
from the Chinese scorpion Buthus martensii Karsch.";
Toxicon 39:407-410(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blanc E., Romi-Lebrun R., Bornet O., Nakajima T., Darbon H.; "Solution structure of two new toxins from the venom of the Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scorpion Buthus martensi Karsch blockers of potassium channels.";
Blochemistry 37:12412-12418(1998).
-:- FUNCTION: Potent blocker of both large-conductance calcium-
activated potassium channels (BKCa channels) and voltage-gated
potassium channels (Kv1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD003588; Charybdotxin; 1.
PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
Neurotoxin; Potassium channel inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOXIN BMTX2.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F19AA7351B9708B8 CRC64;
                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE OF 22-58, SYNTHESIS, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF208300; AAF63972.1; -.
EMBL; AF247058; AAK73518.1; -.
PDB; 2BMT; 13-JAN-99.
InterPro; IPR001947; Charybdotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
MEDLINE=98400946; PubMed=9730813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6507 MW;
                                                                                                 Buthoidea; Buthidae; Buthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 22-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxin_2;
          01-MAR-2002 (Rel. 41, 01-MAR-2002 (Rel. 41, 01-MAR-2002 (Rel. 41,
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                                                                                    PubMed=9354615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00451;
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SIGNAL
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DISULFID
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Length 58;

Score 36; DB 1; Pred. No. 3.2;

61.0%; 55.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: Blocks potassium channels.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CHANNEL INHIBITORS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ye J., Li Y., Yan Y., Ji Y.; "Isolation, characterization and cDNA cloning of a novel toxin from the Chinese scorpion Buthus martensi Karsch, which acts on potassium
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                                                                                                                                                                                                                                                                                                Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
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A1A1A2C415D456A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1;
                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Toxin BMTX3 precursor (Neurotoxin TX3).
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01-077-1996 (Rel. 34, Last sequence update)
01-077-1996 (Rel. 34, Last annotation update)
                                                                                                                                                             59 AA.
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Pfam; PF00451; toxin_2; 1.
Probom; PP0003586; Charybdotoxin; 1.
SMART; SM00505; Knoti; 1.
PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                             PRT;
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InterPro; IPR003614; Knot1.
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                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Created)
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Ye J., Li Y., Yan Y., Ji Y.,
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55.6%;
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Best Local Similarity
Matches 5; Conserv
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59 AA;
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P50329;
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                          SOYBEANS.
                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizoblum group; Bradyrhizoblum.
NCBL_TaxID=29448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                           Dobert R.C., Breil B.T., Triplett E.W.;
"DNA sequence of the common nodulation genes of Bradyrhizoblum elkanii and their phylogenetic relationship to those of other nodulating bacteria.";
Mol. Plant Microbe Interact. 7:564-572(1994).
-i- FUNCTION: INVOLVED IN GENOTYPE-SPECIFIC NODULATION OF SOYBE-
-i- SUMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00376; mezn, ...
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Nodulation; Nitrogen fixation; DNA-binding.
32 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical transcriptional regulator yahB.
YAHB OR B0316.
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                                                                                                                                                  STRAIN-USDA 94;
MEDLINE-95036537; PubMed-7949325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000551; HTH_MerR. Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U04609; AAA63596.1;
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Best Local Similarity 50.0
Matches 5; Conservative
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                      Bradyrhizobium elkanii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:| ::| ||
137 RSQTSRCTCK 146
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                                                                                                                             SEQUENCE FROM N.A.
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P77700;
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NON_TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 36; DB 1; Length 310; 71.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 H-T-H MOTIF (POTENTIAL).
34866 MW; A3EB895E7F69D60C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                         EMBL; AE000138; AAC73419.1; -.
                                                                                                                                                                                                                                                                                                                                                            EMBL; 073857; AAB18042.1; -.
EcoGene; EG1586; yahb.
InterPro; IPR002197; HTH_F1S.
InterPro; IPR000847; HTH_LYSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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DNA_BIND 22
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229 NTKCQCQ 235
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                                                                            REGULATORS.
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Search completed: August 14, 2002, 15:23:12 Job time: 685 sec

4 NTKCRC 9 ||||:| 235 NTKCKC 240

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Gaps

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Ouery Match
61.0%; Score 36; DB 1; Length 326;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels

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Appli , Appl , Appl , Appl

Sequence 11, Sequence Sequence Sequence 1

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GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: TOH, Naoto
APPLICANT: YOURBHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 59; DB 2; Length 119; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 10; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/219,2378
FILIGN DATE: 28-MAR-1994
CLASSIFICATION: 435
US-09-180-100-11
US-09-180-100-22
US-09-2013-895A-3
US-09-2013-895A-3
US-09-008-640-66
US-09-013-895A-2
US-09-013-895A-2
US-08-089-458B-6
US-08-097-827-7
US-08-097-827-7
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-147-784-2
US-08-195-967-2
US-08-105-967-2
US-08-105-967-2
US-08-105-967-2
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US-08-105-967-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILLING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516762
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NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 51671
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119 amino acids TYPE: amino acid
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Sequence 14, Appl
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                                                                                                                                                                                                   August 14, 2002, 15:17:02 ; Search time 82.88 Seconds (without alignments) 2.947 Million cell updates/sec
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\cgn2_6/ptodata/2/laa/5A_COMB.pep:*
\cgn2_6/ptodata/2/laa/5B_COMB.pep:*
\cgn2_6/ptodata/2/laa/6A_COMB.pep:*
\cgn2_6/ptodata/2/laa/6A_COMB.pep:*
\cgn2_6/ptodata/2/laa/RB_COMB.pep:*
\cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
\cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-795-445A-45

US-08-795-445A-45

US-08-795-445A-45

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US-08-795-446A-45

US-08-795-443A-19

US-08-152-443A-19

US-08-152-443A-19

US-09-55-1708-34
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US-08-409-338-1
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US-09-290-640-2
US-09-006-353A-7
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US-09-180-100-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                    GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                - protein search, using sw model
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length: 2000000000
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59
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Match 1
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Maximum DB
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100.0%; Score 59; DB 4; Length 119; 100.0%; Pred. No. 0.01;
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Patent No. 627098
GENERAL INFORMATION:
APPLICANT: ITCH, Naoto
APPLICANT: TOOKEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                       OPERATION SYSTEM: PC-1005/MS-1005
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U1 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION NUMBER: U1 94039
FILING APPLICATION NUMBER: U1 9129
FILING APPLICATION NUMBER: U1 91399
FILING APPLICATION NUMBER: U1 90339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: WALLACH-12A TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 5:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STRRET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 100.0
Matches 10; Conservative
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STRANDEDNESS: single
NUMBER OF SEQUENCES: 8
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US-08-468-560C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY_AGENT INFORMATION:
NAME: TOWNSEANG G. KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELECHHONE: 202-628 5197
TELEFAX: 202-737-3528
                                                       Sequence 14, Application US/08477347

Sequence 14, Application US/08477347

Patent No. 623246

GENERAL INFORMATION:
APPLICANT: BIEDA, Jacek
APPLICANT: BELEGAY, Jacek
APPLICANT: BELETSKY, IGOR
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STRRET: 419 Seventh Street, N.W.
CITY: Washington
STRRET: OC.
COUNTRY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                        RESULT 2
US-08-477-347-14
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US-08-476-862-5
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22040-0747

APPLICANT: ENGELMANN, Hartmut TITLE OF INVENTION: TNF INHIBITORS

Sequence 5, Application US/08476862
Patent No. 626239
GENERL INFORMATION:
APPLICANT: BICDA, Jacek
APPLICANT: BELETKY, IGOT
APPLICANT: BELETKY, IGOT
APPLICANT: BELETY, IGOT
APPLICANT: BELETY, IGOT
APPLICANT: BELETY, IGOT

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Query Match 100.0%; Score 59; DB 4; Length 143; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 10; Conservative 0; Mismatches 0; Indels
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US-09-180-100-15

Sequence 15, Application US/09180100

Patent No. 6306395

GENERAL INPORMATION:
APPLICANT: NARAWURA, Shigekau
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P

CURRENT FILING DATE: 1998-11-02

EARLIER APPLICATION NUMBER: PCT/JP97/01502

EARLIER APPLICATION NUMBER: PCT/JP97/01502

SOFTWARE: PATENTING DATE: 1997-05-01

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

LENGTH: 157

TYPE: PRT
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GENERAL INC. 0300393)
GENERAL INCORNATION:
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REPERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1999-105-01
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 144
    TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
                  FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 143
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US-09-180-100-21
Sequence 21, Application US/09180100
; Patent No. 6306395
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Best Local Similarity 100.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT APPLICATION NUMBER: PCT/JP97/01502
EARLIER APPLICATION NUMBER: PCT/JP97/01502
BARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO SEQ ID NOS: 26
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REPENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAWURA, No. 6306395io
APPLICANT: NAGATA, Shigekazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-180-100-9; Sequence 9, Application US/09180100; Patent No. 6306395
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: protein
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-180-100-9
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76 RTQNTKCRCK 85
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US-09-180-100-10
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Ouery Match 100.0%; Score 59; DB 3; Length 219; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVEWION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-795-445A-45; Sequence 45, Application US/08795445A; Patent No. 6284485
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NAME: Winter, Robert B.
REFERENCE/POCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                             ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: F.
INFORMATION FOR SED ID NO. 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RTQNTKCRCK 130
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         FILING DATE:
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                                                                                                                         100.0%; Score 59; DB 4; Length 157; 100.0%; Pred. No. 0.013; 1. Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59; DB 4; Length 159; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAKAMURA, No. 630639510
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
FARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/08974022; Patent No. 6015938; GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J. APPLICANT: Cacey, David L. APPLICANT: Cacey, David L. APPLICANT: Chang, Ming-Shi TITLE OF INVENTION: OSTEOPROTEGERIN WINBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-DEC-1995
GLASSFIECATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09180100
Patent No. 6306395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 10; Conservative
; ORGANISM: Homo sapiens US-09-180-100-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-180-100-23
                                                                                                                                                                                                                                                                                              105 RTQNTKCRCK 114
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ZIP: 91320-1789
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US-09-180-100-23
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LENGTH: 159
TYPE: PRT
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ZIP: 91320-1789
ZIP: P1320-1789
ZIP: P1320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PAPPLICATION Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/974,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08795446B

Sequence 45, Application US/08795446B

Patent No. 6288032

GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Cacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
TILE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
CORRESPONDENCES: 53
CORRESPONDENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/577,788
                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/POCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET UMBER:
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    LENGTH: 219 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-186-45
                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Thousand Oal STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-795-446B-45
                                                                     FILING DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY. USA
ZIP: 91362-1789
ZIP: 91362-1789
COMPUTER READBLE FORM:
MEDIUW TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
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Patent No. 6284740
GENERAL INPORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Cacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi,
TILLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                              APPLICANT: BOyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              US-08-795-447A-45
; Sequence 45, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                         STREET: One Amgen Center Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Amgen Inc.
1840 Dehavilland Drive
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-795-447A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 18
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US-09-527-236A-3
Sequence 3, Application US/09527236A
Facent No. 6558508
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Tan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REPERENCE: PR375P1
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT APPLICATION NUMBER: 00/00-03-16
PRIOR APPLICATION NUMBER: 00/052,991
PRIOR PILING DATE: 1997-06-11
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR PILING DATE: 1999-03-14
PRIOR PILING DATE: 1999-03-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 3
Ouery Match

100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%; Score 59; DB 4; Length 281; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 14, 2002, 15:17:03 Job time: 686 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-3
                                                                                                                        1 RTQNTKCRCK 10
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121 RTQNTKCRCK 130
                                                                                              1 RTQNTKCRCK 10
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August 14, 2002, 15:15:34; Search time 230.21 Seconds (without alignments) 4.825 Million cell updates/sec
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          747574 segs, 111073796 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                 US-09-499-662-1
59
1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                  Title:
Perfect score:
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Maximum DB seq
                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                       Sequence:
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                                                                                                   Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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11: /SIDS1/gcgdata/hold-genesegy/genesegp-embl/AA1981.DAT:*
12: /SIDS1/gcgdata/hold-genesegy/genesegp-embl/AA1989.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Fas epitope recogn	Human Fas epitope,	Human Fas extracel	Human Fas peptide	Human Fas epitope,	Fas	Fas	Human Fas antiqen	Fas	Rat Fas receptor.	Human Fas receptor
SUMMARIES	ΩI	AAW83030	AAB14740	AAW90890	AAW83053	AAB14761	AAW90911	AAY69517	AAW50286	AAW50288	AAB36228	AAB36229
	DB	19	21	21	F	21	21	21	18	18	21	21
	Length	10	10	10	k	20	20	20	144	159	170	173
of	Query e Match Length DB 1	100.0	100.0	100.0	190	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	59	59	52	59	53	29	59	59	59	59	59
	Result No.	-	7	3	ļ	S	ø	7	8	6	10	11

97JP-0276064. 97JP-0082953. 97JP-0169088.

08-OCT-1997; 01-APR-1997; 25-JUN-1997;

98AU-0059701.

30-MAR-1998;

Fas protein. Unid Human Fas. Homo s Fas-delta-TW Hom	I.	Soluble Fas recept Human Fas receptor	cel	Human Fas protein.	Human Fas antigen.	hFas from plasmid	Human Fas antigen.	Fas protein. Mamm	Amino acid encodin	_	CD-95 (FAS/APO-1)	Human tumour necro	Human Fas antigen	Antigenic peptide	Expression vector	Fas antigen #1. S	Human TNFR1 protei	Plasmid fragment p	Murine Fas. Mus m	Murine Fas antigen	mFas sequence. Sy	Fas ligand (FasL)	Amino acid sequenc	Expression vector	Fas antigen #2. S	Human colon cancer	A human interphoto	Human interphotore	tvb polypeptide.	Human APORP protei
AAB66978 AAB26982 AAB76238	AAR99682	AAM98070 AAR50893	AAR28084	AAR78606	AAR99681	AAR92528	AAW50289	AAW49104	AAB19341	AAB36267	AAB01335	AAB50517	AAW50287	AAW60037	AAR78610	AAR92526	AAW64484	AAR78612	AAR41688	AAR78611	AAR92530	AAW86241	AAB19344	AAR78613	AAR92527	AAB53420	AAY93336	AAY57089	AAW41360	AAW93577
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ALIGNMENTS

scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy. Fas; epitope; HFE7A; monoclonal antibody; humanised antibody; human; apoptosis; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; Fas epitope recognised by MAb HFE7A. AAW83030 standard; Peptide; 10 AA. (first entry) 15-MAR-1999 Homo sapiens AU9859701-A. 08-OCT-1998. AAW83030; RESULT AAW83030 ~

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08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;
FERM-BP-5828; humanised antibody; complementarity determining region;
CDR: Fas ligand; apoptosis modulator; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                 used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                          This peptide represents the human Fas epitope recognised by novel murine anti-human Fas monoclonal antibody HFE7A. It was identified by ELISA and competitive assays using peptides (see AAW8043-63) from the extracellular domain of Fas. The epitope is conserved HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These antibodies bind to the Fas epitope. They are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas autoimmune disease (systemic lupus erythematosus, Hashimoto's animal models.
                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                                                                                                                disease, graft versus host disease, Siogrem syndrome, permittions anaemia, Addison's disease, scleroderma, Goodpasture syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiphe sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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                         Jun O, Kimihisa I;
Tohru T;
                        Akio S, Hideyuki H, Hiroko Y, Ju
Masahiko O, Nobufusa S, Shin Y,
                                                                                                                                                    Claim 20; Page 184; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14740 standard; peptide; 10 AA.
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(SANY ) SANKYO CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy. Glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 59; DB 21; Length 10; 100.0%; Pred. No. 0.0033; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 31; 139pp; Japanese.
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98JP-0276882.
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Matches 10; Conservative
(SANY ) SANKYO CO LTD.
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us-09-499-662-1.rag

97JP-0276064. 97JP-0082953. 97JP-0169088.

98AU-0059701.

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30-MAR-1998;
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25-JUN-1997;
                                                                                                           08-OCT-1997;
                AU9859701-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Internation describes a novel numarized anti-ras anticonomial Fas/Fas molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capperposis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-amemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunoadulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (T) induce antiarteriosclerotic, cardiant and hepatropic activity. (T) induce antiarteriosclerotic, cardiant and hepatropic activity. (T) induce composis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's moultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, and transplant rejection. (I) selectively induce it in abnormal cells but selectively induce it in abnormal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the mative ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a human pas extracellular domain peptide fragment described in the method of the invention
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                                          New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human, apoptosis; HFETA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; slogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                         This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitope; HFE7A; monoclonal antibody; humanised antibody;
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                                                                                                          Example reference 6; Page 97; 263pp; English.
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              WPI; 2000-258930/23.
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic peptides P1-P15 (see AAW83043-57) are partial sequences of amino acids 1-157 of the extracellular domain of human Fas, with between 9 and 11 amino acid residues overlapping one another. P16 (see AAW83058) is a negative control having no homology with human Fas. P1-P16 were used in an ELISA, which demonstrated that novel murine anti-human Fas monoclonal antibody HFE7A specifically binds an amino acid sequence contained in P11. The epitope (see AAW83030) was subsequently identified. The invention provides humanised HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat
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                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                     Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 19; 100.0%; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference Example 6; Page 87; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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(SANY ) SANKYO CO LID.
                                                                                                                                                                                 WPI; 1998-543440/47.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RIQNIKCRCK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such diseases.
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98JP-0276882.

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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                     The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
                                                                                                                              Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 59; DB 21; Length 20; I Similarity 100.0%; Pred. No. 0.0061; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Fas extracellular domain antigenic peptide #11.
                                                                                                                                                                                Example 6; Page 30; 139pp; Japanese.
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                          99JP-0278301.
                                                 98JP-0276883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-2000 (first entry)
                                                                            (SANY ) SANKYO CO LTD.
                                                                                                    WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
                          30-SEP-1999;
                                                 30-SEP-1998;
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20-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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This invention describes a novel numarized anti-ras antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas igand system, by binding to Fas on the cell surface, and prevents cappered is in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of them invention have anti-inflammatory, anti-anemic, antidiabetic, anti-inflammatory, carti-anemic, antidiabetic, antinifertility, neuroprotective, antiviral, antiarteriosciarotic, cardiant and hepatropic activity. (I) induce antiarteriosciarotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoinmune hemolytic anemia, sterility, myssthenia gravis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral dependent diabetes mellitus, alleray, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antigense peptide described in the house has a human anti-murine antigense peptide described in the human and merived antigenic peptide described in the house of the artively sequence represents.
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                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing e.g.' inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fp11; Fas fragment; APO-1; CD95; anti-Fas autoantibody; antibody;
modulator; apoptosis; proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                             Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 21; Length 20; 100.0%; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Example reference 6; Page 110; 263pp; English.
                                                                                                                                                                                                                                                                                                                   cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY69517 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the method of the invention.
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                                                                             Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
(SANY ) SANKYO CO LTD.
                                                                                                                                                       WPI; 2000-258930/23
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                                                                             Serizawa N,
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Chiodi F;

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Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                       contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                excluding) the 1st cysteine residue (preferably at least 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 18; Length 1
100.0%; Pred. No. 0.035;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a Fas antigen derivative, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Fas antigen derivative/IgG1 hinge fusion.
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17..159
/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW50288 standard; Protein; 159 AA.
                                                                                                                           (MOCH ) MOCHIDA PHARM CO LTD. ~
(OSAB-) OSAKA BIOSCIENCE INST.
                                                                                96JP-0135760.
                                         97WO-JP01502.
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                                                                                                                                                                                    Nagata S, Nakamura N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residues are deleted).
                                                                                                                                                                                                                             WPI; 1997-558981/51.
N-PSDB; AAV07003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1998
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                                           01-MAY-1997;
                                                                                  02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997;
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  13-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                              transduces an apportotic signal on binding of its ligand, Fabrican an apportotic signal on binding of its ligand, Fas ligand transduces an apoptotic signal on binding of its ligand, Fas ligand (Fast). Fas autoantibodies have been isolated from the serum of healthy blood donors - these may represent an additional mode of regulation of Fas-mediated signals in vivo. The Fas peptides may be used to modulate apoptosis via blocking autoantibody binding to Fas, thereby reducing or increasing Fast binding, which results in inhibition or stimulation of apoptosis. Fp5 (AAX69514) is thus able to induce apoptosis while Fp11 (AAX69515) and Fp9 (AAX69519) are able to block apoptosis while Fp11 (AAX69515) and Fp9 (AAX69516) comprise amino acids which are important for binding of Fas to Fast. The Fas peptides can be used to obtain antibodies containing a Fas binding site. The peptides and antibodies can be used in assay methods to obtain candidate modulators of Fas-mediated apoptosis. The peptides, mixtures of peptides, nucleic acids or proliferation. The peptides, mixtures of peptides, nucleic acids or mithodies are useful for methods of treating proliferative disorders. The disorders that may be prevented or treated include tumours, cancer, postains, type I diabetes, multiple sclerosis, liver cirrhosis and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                 Sequences AAY69514-Y69521 represent peptide fragments of the Fas protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                           Fas peptide fragments useful for the treatment of proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 21; Length 20; llarity 100.0%; Pred. No. 0.0061; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..16
/label= sig_peptide
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/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW50286 standard; Protein; 144 AA.
                                                                                                   (KARO-) KAROLINSKA INNOVATIONS AB.
                                                                                                                                                                                                                                                                                          Claim 3; Page 57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Fas antigen derivative.
                                       98GB-0013194.
99WO-EP04105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis modulation.
                                                                                                                                                                                 WPI; 2000-106082/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RTQNTKCRCK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                              12-MAR-1999;
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15-JUN-1999;
                                         18-JUN-1998;
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Query Match Local

Best Loc Matches

AAW50286;

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AAW50286 RESULT

Peptide Peptide

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Gaps

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Length 144;

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DNA

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173 AA;
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                       Sequence
                                                                                                                                                                                                                                                                     AAB36229;
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
of viral and other diseases
                                                                                                                                      The present sequence encodes a Fas antigen derivative/IgG1 hinge fusion, which contains a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases with as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1; accelerated graft arteriosclerosis; vascular occlusive disease.
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                                                                                                                                                                                                                                                                             Length 159;
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                                                                                                                                                                                                                                                                             Score 59; DB 18;
Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Movva RN,
                                                                                                                     Disclosure; Fig 5; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                              AAB36228 standard; Protein; 170 AA.
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        MOCHIDA PHARM CO LTD.
OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0294176
99US-0307690
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                               10; Conservative
                                    Nakamura N;
                                                                                                                                                                                                                               virus-infected cells
                                                    WPI; 1997-558981/51
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N-PSDB; AAC66557.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 1 RTQNTKCRCK 10
                                                                                                                                                                                                                                                  159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Fas receptor.
                                                               N-PSDB; AAV07005
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10-MAY-1999;
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                                   Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method of gene therapy which involves the use of RasR or FGFR-1 coding sequences to treat vascular diseases. The invention also provides vectors for use in this method. The treatable diseases include vascular occlusive diseases associated with cell proliferation, such as accelerated graft arteriosclerosis and other forms of stenosis.
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proliferation, comprises transferring, to cells or progenitors, the sequence encoding Fas antigen or receptor, or the fibroblast growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                                       Disclosure; Page 33-34; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36229 standard; Protein; 173 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2000; 2000WO-EP03532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0294176,
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Best Local Similarity
Matches 10; Conserv
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The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGP)-10 modulators and/or platelet activating factor (PRF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                             Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condution; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischemnia; parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock The present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLB) a graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis. Alzheimer's disease, anorexia.
100.0%; Score 59; DB 21; Length 173; 100.0%; Pred. No. 0.041; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Senaldi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calzone FJ, Chang M,
                                                                                                                                                                                                                       AAB66978 standard; Protein; 219 AA.
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                                                                                                                                                                                                                                                                                                      (first entry)
                                     10; Conservative
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                                                                                                                     121 rtgntkcrck 130
Query Match
Best Local Similarity
                                                                               1 RTONTKCRCK 10
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                                                                                                                                                                                                                                                                                                                                            Fas protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is Fas, a member of the tumour necrosis factor receptor family. A novel human tumour necrosis factor receptor, designated TR9, has been isolated The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for treating, preventing or diagnosing common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
                                                                                                                                                                                                                                                                                                                                             Human; Fas; tumour necrosis factor; TR9 receptor; immunosuppressive; antidiamatory; cardiant; antiasthmatic; antidiabetic; antiallergic; antiathritic; antirheumatic; anti-HTV; anticonvulsant; cytostatic; neuroprotective; gene therapy; Death Domain Containing Receptor 6; common variable immunodeficiency; X-linked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Addrich syndrome; autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data.
                                         Gaps
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     Length 219;
                                       0; Indels
   100.0%; Score 59; DB 22;
100.0%; Pred. No. 0.051;
ive 0; Mismatches 0;
                                                                                                                                                                                                       AAB26982 standard; Protein; 281 AA
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                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
                                       Conservative
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                                                                                                             121 rtqntkcrck 130
Query Match
Best Local Similarity
Matches 10; Conser
                                                                           1 RTQNTKCRCK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                               Human Fas.
                                                                                                                                                                                                                                         AAB26982;
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1 RTQNTKCRCK 10

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A natural, soluble Fas antigen variant (AAR99682), designated Fas dell, and other Fas variants (AAR99683-85) are derived by alternative splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for the variant was obtd. from human peripheral blood mononclear cells. The Fas dell variant lacks the transmembrane domain of insoluble Fas antigen (AAR99681). Recombinant dell variant, or fragments of it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells. Detection of increased levels of soluble forms of Fas antigen can be used to diagnose autoimmune diseases, esp. systemic lupus erythematosus and angioimmunoblastic lymphadenopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE; angioimmunoblastic lymphadenopathy; AILD.
                                                                                                                                                                                                                                                                                                                                            "preferred peptide from breakpoint region"
                                                                                                                                                                                                                                                                                                                                                                           /note= "preferred peptide from breakpoint region"
                                                                                                                                                                                                                                                                                                  /note= "preferred peptide from breakpoint region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing – used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus
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                                                                                                                                                              /note-
17..168
/label=Extracellular_domain
/note= "the 5 C-terminal residues of the
Fas antigen extracellular domain
deleted in Fas dell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 0.07;
                                                                                                                           17..314
/label= Mat_protein
/note= "soluble Fas dell antigen"
                                                                                                                                                                                                                                                                                                                  (claim 4, page 132)"
                                                                                                                                                                                                                                                                     /label= Cytoplasmic_domain
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Job time: 832 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 114-16; 152pp; English.
                                                                                               1.16
/label= Sig_peptide
                                                                               Location/Qualifiers
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100.0%;
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161..171
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Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAT34527.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             WO9620206-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                 Key
Peptide
                                                                                                                            Protein
                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCF product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. The insert sequence of pBluescript-Fas-delta-TM encoded the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                    Fas-delta-TM; transmembrane deletion; apoptosis; antibody; adoptive immunotherapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig. 3-1 to 3-4; 38pp; English.
                                                                                                                                                                                                                                                                                                                1..16
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shapiro JP;
                                                                                          AAR76238 standard; Protein; 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0152443.
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                                                                                                                                                        (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAQ93879.
                121 rtgntkcrck 130
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 06-NOV-1995
                                                                                                                                                                                       Fas-delta-TM
                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                         AAR76238;
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AAR99682

XEXEXEX

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

August 14, 2002, 15:18:58 ; Search time 108.64 Seconds (without alignments) 8.845 Million cell updates/sec Run on:

US-09-499-662-1 59 Perfect score: Title:

1 RTONTKCRCK 10 Sequence: BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir_71:*
1: pir1:*
2: pir2:*
!: pir3:*
: pir4:*.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	FAS soluble protei	antiqen	G)	apoptosis-mediatin	gene ox40 protein	OX40 homolog - hum		protein -	tumor necrosis fac	hypothetical prote	_	н	cytochrome c552 NM	probable transcrip	hypothetical prote	int-1-like protein	hypothetical prote	^	c	charybdotoxin 2 -	trans-activating t	ORF MSV142 probabl	16K vascular endot	grain softness pro	softness	netical pr	>	neuraminidase - in	exo-alpha-sialidas
SUMMARIES	£ £	137383	JC2395	A40036	A46484	I48700	137552	I50610	B36470	GQMST1	T09052	D90674	G85524	F81938	D64758	T23462	S00834	C69941	A27340	A60963	B60963	TNLJND	T28303	D49530	S51770	S48186	T18066	C69255	S20711	NMIV3
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ф	Query Match	100.0	100.0	100.0	86.4	66.1	66.1	62.7	62.7	62.7	62.7	61.0	61.0	61.0	61.0	59.3	59.3	59.3	59.3	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6
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exo-alpha-sialidas protein C18H9.7 {i	hypothetical prote hypothetical prote	box A-binding fact chromosome segrega	alpha tectorin – c ornatin A2 – leech	ornatin A3 - leech mast cell degranul	metallothionein is	hypothetical prote protein F3F9.8 {im	polyprotein (clone	cold-regulated pro	hypothetical prote
NMIV F88188	T23090 T23738	S40382 B97116	T30243 S19566	S19621 MDHB	S59073	S08640 F96812	PQ0245	B45512	T47433
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30 31	33.2	34 35	36 37	8 6 6 6	40	4 4 1 2 1	43	44	45

ALIGNMENTS

RESULT 1 137383 FAS soluble protein - human C; Species: Homo saptens (man) C; Species: Homo saptens (man) C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000 C; Caccession: 137383 R; Cascino, I; Fiucci, G; Papoff, G; Ruberti, G. J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule A;Reference number: 137383; MUID:95181785 A;Accession: 137383
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molacule type: mRNA A:Residues: 1-314 cRES>
A;Cross-references: EMBL:247993; NID:9728578; PIDN:CAA88031.1; PID:9695539

Gaps ; 0 Query Match 100.0%; Score 59; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 0.0073; Matches 10; Conservative 0; Mismatches 0; Indels

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121 RTQNTKCRCK 130 1 RTQNTKCRCK 10 δ

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Fas antigen precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat 1
A;Reference number: JC2395; MUID:94128114

A;Molecule type: mRNA A;Residues: 1-324 'KIM> A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468 A;Experimental source: thymus A;Accession: PC2246

A;Molecule type: mRNA A;Residues: 1-62,'RPT' <KI2> A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468 A;Experimental source: liver C;Genetics:

A; Introns: 62/1 C; Superfamily: NGF receptor repeat homology C; Keywords: transmembrane protein F; 1-21/Domain: signal sequence #status predicted <SIG>F; 22-324/Product: Fas antigen #status predicted <MAT>

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A; Accession: A46484
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1.327 (xMar)
A; Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A; Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g19326
A; Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g19326
A; Racchi, M.; Watanabe-Fukunaga, R.; Nagata, S.
B; Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
B; Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
A; Title: Aberrant transcription caused by the insertion of an early transposable elem A; Reference number: A47254; MUID:g3189576
A; Accession: A47254
A; Accession: A77254
A; Accession: A77254
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Accession: A46484; A47254 R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki, Immunol. 148, 1274-1279, 1992 A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas A;Reference number: A46484; MUID:92148151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anolecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Residues: 1-96 <ADA>
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Cross-references: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268
C;Superfamily: NGF receptor repeat homology
C;Reywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG6>
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N;Alternate names: OX40 antigen
C;Specias: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision O2-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A;Reference number: 148700; MUID:94044750
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-272 < RESS
A; Cross-references: EMBL:221674; NID:9312827; PIDN:CAA79772.1; PID:9312828
A; Cross-references: EMBL:221674; NID:9312827; D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
Eur. J. Immunol. 25, 926-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX A; Reference number: 148334; MUID:95255413
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A;Cross-references: EMBL:X85214; NID:9732818; PIDN:CAA59476.1; PID:9732819
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 16;
2; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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Similarity 66.7%;
6; Conservative
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X63717; NID:928741; PID:928742
R;Ochm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member A;Reference number: A38142; MUID:92268122
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A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
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                                                                                                                                                                        Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis-mediating membrane-associated polypeptide Fas - mouse C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Status: preliminary; not compared with conceptual translat A; Molecule type: nucleic acid A; Residues: 1-134, 'Q', 136-335 A; Experimental source: SWM6, Cells A; Note: sequence extracted from NCBI backbone (NCBIP:103810) A; Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis-mediating surface antigen Fas precursor - human N,Alternate names: surface antigen APO-1
   F;44-79/Domain: NGF receptor repeat homology <NGF> F;81-124/Domain: NGF receptor repeat homology <NG4> F;171-188/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                    Query Match 100.0%; Score 59; DB 2; L. Best Local Similarity 100.0%; Pred. No. 0.0075; Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Krammer, P.H. submitted to the EMBL Data Library, February 1992
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A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
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A, Accession: S24543
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-335 <KRA>
                                                                                                                                                                                                                                                                                                                                   117 RTQNTKCRCK 126
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Best Local Similarity
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Gaps

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Length 360; Indels

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N.Alternate names: tumor necrosis factor receptor, 55K
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1992 #text_change 01-Dec-2000
C; Accession: A38634; B40254; S16677; S19021; I554525; I57826
R; Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A; Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A; Reference number: A38634; MUID: 91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro A;Reference number: $16677; MUID:91285014 A;Accession: $16677
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A/Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A/Reference number: 154532; MUID:94245292
                          A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                                                                       RimcMahon, J.A.; McMahon, A.P.
Development 107, 643-650, 1989
A;Title: Nucleotide sequence, chromosomal localization and developmental expression A;Reference number: A43558; MUID:90126394
A;Reference number: A43558
A;Status: preliminary; not compared with conceptual translation
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Pred. No. 44;
1; Mismatches
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44;
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A; Residues: 1-360 <MCM>
C; Superfamily: int-1 transforming protein
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66.78;
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Best Local Similarity
Matches 6; Conserv
                                                        A; Molecule type: mRNA
A; Residues: 1-360 <GAV>
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A; Residues: 1-454 <GO2>
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A; Residues: 1-454 <BAR>
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319 TRMTKCECK 327
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A; Residues: 1-454 <ROT>
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A:Accession: B36470
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                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C; Accession: 137552
R; Latza, U; Durkop, H; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
Eur. J. Immunol. 24, 677-683, 1994
A; Titler: The human OX40 homolog: cDNA structure, expression and chromosomal assignment characteries on number: 137552; MUID:94170844
A; Reference number: 137552
A; Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Gallus gallus (chicken)

C, Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C; Accession: 156610; S33350

R; Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, A: Timunol. 154, 4485-4494, 1995

A; Title: Identification and analysis of the expression of CD8 alpha and CD8 alpha appropries.
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C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 15-Jun-1996
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 15-Jun-1996
C;Datesion: B36470; A43558
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult in A;Reference number: A36470; MUID:91122634
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A.Raccession: 150610
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-235 <TRE>
A.Cross-references: EMBL:222726; NID:9488149; PIDN:CAA80421.1; PID:9297781
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Steporfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 16;
2; Mismatches 1; Indels
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Pred. No. 32;
3; Mismatches 2; Indels
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A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA535°
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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N;Alternate names: int-1 related protein
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50.0%;
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66.7%;
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Matches 6; Conservative
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208 KTRRRCRCK 217
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102 TQDTVCRCR 110
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Best Local Similarity
Matches 5; Conserv
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                                                                                   98 TODTVCRCR 106
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                          TONTKCRCK 10
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61.08;
71.48;
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conserv
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5 NTKCQCQ 11
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                                                                                                A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G', 395-454 (RE2>
A;Residues: 1-393,'G', 395-454 (RE2>
C;Coment: This protein is one of two distantly related receptors for both TNF-alpha (ca C;Genetics:
A;Gene: TNFR-2
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09052
R;Habuchi, T.: Luscombe, M.; Elder, P.A.; Knowles, M.A.
Geomanics 48, 277-288, 1998
A;Title: Structure and methylation-based silencing of a gene (DBCCRI) within a candidate A;Reference number: Z16537; MUID:98207242
A;Accession: T09052
                                                                                                                                                                                                                                                                                       A; Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C; Superfamily: tumor necrosis factor receptor; dyoprotein; receptor; transmembrane protein
F; 1-29/Domain: signal sequence #status predicted <SIG>F; 30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F; 30-212/Domain: extracellular #status predicted <EXT>
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                                 factor
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis
A;Reference number: 157826; MUID:93156721
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A; Residues: 1-761 < RNB>
A; Cross-references: EMBL: AF027734; NID: g3041876; PIDN: AAC39691.1; PID: g3041877
A; Experimental source: tissue type: brain; developmental stage: fetal and infant C; Genetics:
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Pred. No. 53;
0; Mismatches 2; Indels
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Pred. No. 80;
3; Mismatches
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A;Note: IB3089A
C;Superfamily: human hypothetical protein DBCCR1
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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hypothetical protein 20404 [imported] - Escherichia coli (strain 0157:H7, substrain E C; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: G85524 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: G85524 A; Status: preliminary A; Status: preliminary A; Residues: 1 66 <2700 A; Cross-references: GB:AB005174; NID:912513132; PIDN:AAG54659.1; GSPDB:GN00145; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933 C; Genetics: A; Genetics: Genetic
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
As A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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A; Motecule type: DNA
A; Motecule type: DNA
A; Residues: 1-86 < HAY>
A; Cross-references: GB:BA000007; PIDN:BAB33787.1; PID:g13359821; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
A; Genetics: A; G
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Pred. No. 21;
2; Mismatches
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Job time:
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C;Species: Diodappi #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: D64758
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-310 <BLAT>
A;Cross-references: GB:AE000138; GB:U00096; NID:91786501; PIDN:AAC73419.1; PID:91786508;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Genetics:
A;Gene
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C;Species: Caenorhabditis elegans
C;Deate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23462
A;Reference number: 219744
A;Ccession: T23462
A;Accession: T23462
A;A
C; Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-163/Product: eytochrome c552 #status predicted <MAT> F;28-109/Domain: cytochrome c6 homology cXC6> F;28-109/Domain: cytochrome c6 homology cXC6> F;38,41/Binding site: heme (Cys) (covalent) #status predicted F;42,92/Binding site: heme iron (His, Met) (axial ligands) #status predicted
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Pred. No. 58;
2; Mismatches 0; Indels
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Best Local Similarity 71.4%; Pro
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55.6%;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AF104034; AAD20221.1; ...
INSP; P2594; ICDF.
InterPro; IPR001368; TNFR_c6.
Pfam; PF000205; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00052; TNFR, 19 UNKNOWN_1.
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16644 MW; 7DEC76EC40A6BA4F CRC64;
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100.0%; Pred. No. 0.00026;
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Q96E62
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Q9XZ89
O73822
O73682
Q9LE55
Q9LUQ3
Q9UGG6
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09JJL6
09QZM4
043686
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Q9tsn4 macaca fasc
Q9gk36 macaca assa
Q9bdn4 cercocebus
Q9bdD macaca neme
Q9bdp2 macaca mula
Q9d140 macaca mula
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homo sapien
ovis aries
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Q14293 }
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Score

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Minimum DB : Maximum DB :

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Sequence:

Scoring table:

Searched:

Gaps

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Indels

Length 314;

RESULT Q9GK28

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SEQUENCE FROM N.A.
TISSUB-LYMPHOCYTE;
Trakagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
Trakagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
"Cloning of sheep fas antigen.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB011671, BAA37093.1;
Therpro, IPRO004488; Death.
InterPro, IPRO00488; Death.
InterPro, IPRO01368; TWFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aotus trivingatus (Night monkey) (Douroucouli).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 6; Length 327; 100.0%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00131; death; 1.
Pfam; PF00120; TWFR_c6; 3.
SMART; SM00008; DEATH; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TWFR_MSFR_L; 1.
SROSITE; PS00505; TWFR_NSFR_C5; 2.
SEQUENCE 327 AA; 36928 MW; 5CFEB844B2BE387A CRC64;
                                                    83F8FAC62DB8B457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-BDP0;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                               100.0%; Score 59; DB 4; 1
100.0%; Pred. No. 0.00049;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA.
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PS00652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 2.
314 AA; 35386 MW; 831
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                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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                           PROSITE;
SEQUENCE
  PROSITE;
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MEDLINE=95181785; PubMed=7533181;
MEDLINE=95181785; PubMed=7533181;

"Three functional soluble forms of the human apoptosis-inducing Fas molecule are produced by alternative splicing.";

J. Immunol. 154:2706-2713(1995).

EMBL: Z47993; CAA888031.1; --
HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                        Macaca arctoides (Stump-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH; 1.
PROSITE; PS50052; TNFR_NFR_1; 1.
PROSITE; PS50052; TNFR_NFR_1; 1.
PROSITE; PS50050; TNFR_NFR_1; 1.
SROUENCE 310 AA; 34806 MW; C5C79BFIF804A419 CRC64;
                                                                                                                       09GK28; TEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN APO-1/CD95.
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Last annotation update)
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100.0%; Pred. No. 0.00048;
Live 0; Mismatches 0;
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014293;
01-007-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-DEC-2001 (TrEMBLrel. 19, La
FAS SOLUBLE PROTEIN.
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                                                                                                      PRELIMINARY;
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NCBI_TaxID=9540;
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Matches 10; Conserv
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Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                             Macaca assamensis (Assam's macaque) (Assam's monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chi L., Shui B., Jiang H., He F.O., Zhang Y.R., Cai Y.Y.;
Chi L., Shui B., Jiang H., He F.O., Zhang Y.R., Cai Y.Y.;
Choing and sequencing of bear monkey Fas antigen cDNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
REBL, AF326208; AA64382.1;
RINGEPPOS DESCOURS DEATH.
RINGEPPOS IPRO00488; Death.
RINGEPPOS IPRO00488; TNFR_C6.
REMARY: SMO0005; DEATH.
REMARY: SMO0208; TNFR, 2.
REMARY: SMO0208; TNFR, 2.
REMOSITE; PS50017; DEATH_DOMAIN; 1.
REMOSITE; PS50017; DEATH_DOMAIN; 1.
REMOSITE; PS500505; TNFR_NGFR_1; 1.
REMOSITE; PS500505; TNFR_NGFR_1; 1.
REMOSITE: PS500505; TNFR_NGFR_1; 1.
REMOSITE: PS500505; TNFR_NGFR_1; 1.
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                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN APO-1/CD95.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
                  331 AA
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INTERPORT IRROUGH 88; TWFR_C6.
Pfam; PF00020; TWFR_C6; 2.
SWART; SW00209; TWFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50050; TWFR_NGFR_1; 1.
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                  Q9GK36
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"X MEDLINE-20237686; PubMed-10773350;
"A MENLYAMA Y., Terao K., Inoue-Murayama M.;
"A Murayama Y., Terao K., Inoue-Murayama M.;
"Y Molecular cloning and characterization of cynomolgus monkey Fas.";
"I "Molecular cloning and characterization of cynomolgus monkey Fas.";
"X Molecular cloning and characterization of cynomolgus monkey Fas.";
"X Molecular Cloning and characterization of cynomolgus monkey Fas.";
"X Molecular Cloning and characterization of cynomolgus monkey Fas.";
"X Molecular Cloning and characterization of cynomolgus monkey Fas.";
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Weiss W.R., Ansari A.A.;

"Cloning, sequencing, and homology analysis of nonhuman primate
resyFas-ligand and co-stimulatory molecules.";

I mmunogenetics 53:315-328(2001).

EMBL; AF344835; AAX37531.1; -..

R HSSP; P22445; 1DDF.

R InterPro; IPR001368; TNFR.c6.

R InterPro; IPR001368; TNFR.c6.

R Pfam; PG00200; TNFR, c6.

SMART; SM00000; TNFR, c6.

R SMART; SM00000; TNFR, 1.

R PROSITE; PS50017; DEATH, DOMAIN, 1.

R PROSITE; PS50017; TNFR.NGFR.1; 1.

R PROSITE; PS50055; TNFR.MSFR.2; 2.

R VARANT

157 157
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 59; DB 6; Length 328, 100.0%; Pred. No. 0.00051; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DEATH RECEPTOR FAS (APO-1/CD95).
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Best Local Similarity 100.(
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hes 10; Conservative
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O9TSN4; Q9TSN4 9

RESULT Q9TSN4

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RESULT Q9GK36

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Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                           MEDLINE=21383618; PubMed=11491535;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 90.0°
Matches 9; Conservative
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       Cercopithecinae; Macaca.
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                      NCBI_TaxID=9544;
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Q9GL40
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MEDLINE-21383618; Pubmed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.P., Mayne A.E., King C.L., Genain C.P.,
T. Cloning, sequencing, and homology analysis of nonhuman primate
FaskFas-ligand and co-stimulatory molecules.";
I. Immunogenetics 53:315-328(2001).
REMBL; AF344850; AAK37610.1; -.
REMBL; AF344850; AAK37610.1; -.
REMBL; AF344850; Death.
InterPro: IPR001368; TNFR_C6.
Pfam; PR000002; TRFR_C6; 2.
REMAT; SM00002; TRFR_C6; 2.
REMAT; SM00003; TNFR_C6; 2.
REMAT; SM00208; TNFR_C6; 3.
REMAT; SM00208; TNFR_CFR_C6; 3.
REMAT; SM00208; TNFR_C6; 3.
REMAT; SM00208; TNFR_CFR_C6; 3.
REMAT; SM00208; TNFR_C6; 3.
REMAT; SM00
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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R -> H.
R -> S.
E -> G.
G -> A.
E -> G.
C -> A.
E -> G.
M; ID843C4DEID343F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           09BDNO, PRELIMINARY; PRT; 331 AA. 09BDNO; 10.1-JUN-2001 (TrEMBLrel. 17, Created) 01.-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) FAS ANTIGEN CD95.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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60 R
61 N
77 E
95 G
282 E
298 G
300 C
37277 MW;
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NCBI_TaxID=9545;
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331 AA;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Shui B., Chi L., Zhang Y.R.;
Shui B., Chi L., Zhang Y.R.;
Shui B., Chi L., Zhang Y.R.;
Cloning and sequenching of Rhesus monkey Fas antigen cDNA.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

R HSSP; PS245; IDDF.
R InterPro; IPR000488; Death.
R InterPro; IPR001368; TNFR_c6.
R Pfam; PF00020; TNFR_c6; 2.
R SMART; SM00005; DEATH; 1.
R SMART; SM00208; TNFR, 2.
R PROSITE; PS50017; DEATH_DOMAIN; 1.
R PROSITE; PS50017; DEATH_DOMAIN; 1.
R PROSITE; PS00505; TNFR_C6F_2; 2.
C SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;
Merss, w.r., fautaria. A.c., "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).

Immunogenetics 53:315-328(2001).

Immunogenetics 53:315-328(2001).

Interpro; PR000488; Death.

Interpro; IPR000488; Death.

Interpro; IPR000488; TNFR_c6.

Pfam; PF00002; TNFR_c6, 2.

SMART; SM00005; DEATH; 1.

SMART; SM000208; TNFR: 2.
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PROSITE; PS50017; DEATH_DOMAIN, 1.

PROSITE; PS50052; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; 2.

VARIANT 75 75 75 V -> A.

VARIANT 89 89 E -> K.

VARIANT 196 196 E -> K.

VARIANT 201 201 R -> H.

SEOUGNCE 333 AA; 37468 MW; 98C17F766762F287 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN.
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RESULT 12 Q9DCQ1

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A ISONO T., Tanbe Y., Nagano Y., Seto A.;

I Splicing and allelic variation in the rabbit Fas antigen gene.";

Submitted (DEC.1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB021298; BAA78430.1; -.

HSSP; P25445; 1DDF.

R InterPro; IPR000488; Death.

R InterPro; IPR00188; Death.

R InterPro; IPR00188; TNFR.c6.

Pfam; PF00531; death; 1.

R Pfam; PF00050; TNFR.c6.

R PART; SM0005; DEATH; 1.

R SMART; SM0005; DEATH; 1.

R PROSITE; PS50017; IDRATH_DOMAIN; 1.

R PROSITE; PS50050; TNFR_NGFR_1; UNKNOWN_1.

R PROSITE; PS50050; TNFR_NGFR_2; 2.

SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;
                                                                                        SEQUENCE FROM N.A.

ISONO T., Tanbe Y., Nagano Y., Seto A.;

ISONO T., Tanbe Y., Nagano Y., Seto A.;

Splicing and allelic variation in the rabbit Fas antigen gene.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AB021297; BAA78429.1; -.

HNSSP; 014763; 1D4V.

InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 3.

SMART; SM00208; TNFR_C6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryccolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 263;
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100.0%; Pred. No. 0.041;
iive 0; Mismatches 0; Indels
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      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B-TYPE FAS ANTIGEN.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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Best Local Similarity 100.0
Matches 8; Conservative
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SEQUENCE FROM N.A.
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                                 NCBI_TaxID=9986;
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09XS60; (TEMBLrel. 12, Created)
01-NOV-1999 (TEMBLrel. 12, Last sequence update)
01-NOV-1999 (TEMBLrel. 19, Last annotation update)
FAS ANTIGEN SPLICED VARIANT.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TCBI_TaxID=10090;
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBE. AKO02599: BAB22211.1;
HSSP: P25445; IDDF.
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88.9%; Pred. No. 0.02;
Live 1; Mismatches 0; Indels
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PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 327 AA; 37437 MW; D8DA95CA525CED56 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER
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STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
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InterPro; IPR000488; Death.
InterPro; IPR001368; TWFR_C6.
Pfam; PF00020; TWFR_C6; 3.
SWART; SW0005; DEATH; 1.
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AC AC DIT DIT DIT OC OC

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE C-TYPE RSA ANTIGED.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Manmalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OC Manmalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NOBI_TaxID-9986;

RN 113

RN 52UUENCE FROM N.Y.

RA ISONO T., Tanbe Y., Nagano Y., Seto A.;

R. Splicing and allelic variation in the rabbit Fas antigen gene.";

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:15:33 ; Search time 230.21 Seconds (without alignments) 37.634 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

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747574 seqs, 111073796 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

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Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Anti-Fas humanised	Anti-Fas MAb HFE7A	Mouse anti-Fas ant	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas				
QI	AAW83031	AAW83032	AAW83033	AAW83034	AAW83035	AAW83042	AAB14748	AAB14772	AAB14773	AAB14774	AAB14777
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Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	205	205	205	205	205	205	205	205	205	205	202
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AAB14778 AAW90898 AAW90922 AAW90923 AAW90924 AAW90928	AAW90931 AAW90931 AAY23781 AAY18123 AAR70202 AAR70202	AAR70189 AAR23767 AAR18120 AAR33309 AAR85197 AAP90541	AAR55127 AAR60302 AAR60306 AAR24575 AAR71895 AAR713563 AAW13563 AAW75355 AAY73771 AAY78118
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ALIGNMENTS

AAW83031 standard; Protein; 238 AA. 15-MAR-1999 (first entry) AAW83031;

AAW83031 RESULT

Anti-Fas humanised antibody HFE7A light chain HH type

HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic luqus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; actoriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

Location/Qualifiers
1..20
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21..238
/label= Mat_protein
21..131
/label= Variable
132..238
/label= Constant Peptide Protein

Region Region

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chain of murine anti-human Fast and antibody HFETA.

Chain of murine anti-human Esquence (see AAM83042) entailed making P47A, K49R, H80S, P81R, V82L, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised HH type HFETA light chain and DNA encoding the region of human communoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA approxal, in abormal cells expressing Fas, and of inhibiting apoptosis in normal cells expressing Fas, and of inhibiting are used to evaluate, in animal models, treatments of diseases that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, Sjogren syndrome, pernicious anaemia, Addison's disease, recorderma, Goodpasture syndrome, Crohn's disease, theumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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S, Shin Y, Tohru T;
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44..58
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74..80
/label-CDR_L2
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113..121
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Query Match 100.0%; Score 205; DB 19; Length 238; Best Local Similarity 39.7%; Pred. No. 1.2e-05; Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

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61 XXXXXXXXQQSNEDPRT 78
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepetitis and AIDS
                                                                                                                                                               HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; slogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune hemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; actoriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                            Anti-Fas humanised antibody HFE7A light chain HM type.
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Nobufusa S, Shin Y, Tohru T;
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       Chain of murine and sequence to the murine in munication of the murine sequence (see AAW83042) entailed making chain of murine anti-human Fass monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making the ATA and K49R antion coid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coli pHSGHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion of fragment of the humanised HM type HFE7A light chain and DNA encoding the region of human immunoglobulin Kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised antibodies by culturing host cells. Humanised antibodies are used to evaluate, in animal cells are capable of inducing apoptosis in abnormal cells. REFA, are capable of inducing apoptosis in abnormal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune craft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatchia removing multimine haemolytic anaemia, continity.
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This is the amino acid sequence of the HM type humanised light
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 238;
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47; Mismatches 0;
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This is the amino acid sequence of the MM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli saw 73697 harbors plasmid pHSGMMC carrying a fusion fragment of the humanised wat type HFE7A light chain and DNA encoding the region of human kappa chain, and is deposited as FERM BP-6071 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), clike native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in cormal cells. The humanised antibodies are used to evaluate, in theractions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease.
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thrombopenia purpura and insulin-dependent diabetes), allergies,
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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                Anti-Fas humanised antibody HFE7A light chain PDHH type.
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S, Shin Y, Tohru T;
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/label- Mat_protein
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                       AAW83034 standard; Protein; 238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR_L3
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97JP-0082953.
97JP-0169088.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .121
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                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
                                                                       15-MAR-1999
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25-JUN-1997;
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Masahiko O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU9859701-A.
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                                              AAW83034;
                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                  Protein
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            AAW83034
RESULT
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chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making
D1E, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
amino acid substitutions; these residues are conserved in the
human light chain (kappa chain). Host cell Escherichia coli
pHSHHS SANK 7039B harbors plasmid pHSHH5 carrying a fusion
fragment of the humanised PHHH type HFE7A light chain and DNA
cencoding the region of human immunoglobulin kappa chain, and is
deposited as FERN BP-6274 (claimed). The invention provides
methods for producing humanised antibodies by culturing host
cells. Humanised versions of HFE7A (see AAM8301-37), like native
HFE7A, are capable of inducing apoptosis in abnormal cells
expressing Fas, and of inhibiting Fas-induced apoptosis in normal
colls. The humanised antibodies are used to evaluate, in animal
models, treatments of diseases that involve Fas/Fas ligand
interactions, and also to treat such diseases, including autcimmune
clistoper producing and cliptose syndrome, pernicious anaemia,
disease, rheumatoid arthritis, autcimmune haemolytic anaemia,
disease, rheumatoid arthritis, autcimmune haemolytic anaemia,
disease, rheumatoid arthritis, autcimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashlmoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-Fas humanised antibody HFE7A light chain PDHM type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 205; DB 19; Best Local Similarity 39.7%; Pred. No. 1.2e-05; Matches 31; Conservative 47; Mismatches 0;
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/label= Mat_protein
21..131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
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Matches
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CHain of murine anti-human Fas monoclonal antibody HFE7A.

CHAIN K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native KFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas,Fas ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
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S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 220-221; 292pp; English.
                                                                                                                                                /note= "claim 9"
74.80
/label= CDR_L2
'label= Variable
                                                             label= Constant
                                                                                                                                                                                                                                                 "claim 9"
                                                                                                                                                                                                                                                                                                        /label= CDR_L3
/note= "claim 9"
                                                                                          44..58
/label= CDR_L1
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N-PSDB; AAV70078.
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25-JUN-1997;
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis; HEFA; autoinmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; sjoren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                                                                                                                                                                                                                                              HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
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S, Shin Y, Tohru T;
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/note= "claim 9"
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/label= CDR_L1
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97JP-0082953.
97JP-0169088.
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15-MAR-1999 (first entry)
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100.0%; Score 205; DB 19; Length 238; 39.7%; Pred. No. 1.2e-05; ive 47; Mismatches 0; Indels 0

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                                                                                             This is the amino acid of the light chain of murine anti-human Fas monoclonal antibody HFE7A. CDNA (see AAV70130) encoding the light chain was obtained from HFE7A-secreting hybridoma (FEMR BP-588).

RNA by RT-FCR (see AAV70127-28). The invention provides humanised HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These artibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's disease (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, 50gren syndrome, pernicious anaemia, Addison's disease, reumatoid arthitis, autoimmune haemolytic anaemia, sterility, myaathenia arthitis, autoimmune haemolytic anaemia, sterility, myaathenia and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypopiastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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                                        Reference Example 4; Page 189-190; 292pp; English.
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                                                                  The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
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Example 4; Page 70; 139pp; Japanese.
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                                                                                   (complementarity determining regions) to antibody HEE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (pannyalophihisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and ABB14777-H14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-Inman Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
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                                                                                                                                                                                            antibodies
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                                                                                                                                                                                                                                  Sequence
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interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, apportantly, aplastic anaemia (pannyalophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and ABB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Iigand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                          Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-Fas antibody light chain, SEQ ID NO:107.
                                                                                                                                                                                                          Score 205; DB 21; red. No. 1.2e-05;
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                          Pred. No. 1.26
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 101; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14777 standard; Protein; 238
                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                          100.0%;
39.7%; F
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                                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Mus musculus.
Chimeric - Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SANY ) SANKYO CO LTD.
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                                                                                                                                                        238 AA;
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-Fas antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2000169393-A.
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                                                                                                                      antibodies
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                                                                                                                                                         Sequence
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Best Local 9
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             glomerulonephritts, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the FasYFas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                       Gaps
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cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised anti-Fas antibody light chain, SEQ ID NO:109.
                                                                                                                                                                DB 21;
                                                                                                                                                                                                    ö
 myocarditis,
                                                                                                                                                              100.0%; Score 205; DB 21
39.7%; Pred. No. 1.2e-05;
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 103; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB14778 standard; Protein; 238 AA.
 allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0278301.
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                           AA;
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                                                                                                         238
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                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosupressive, thyronimetic, antirchiammatory, antisheumatic, nephrotropic, antilefractility, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
represent the light chains of several humanised {\tt HFE7A}-derived anti-Fasantibodies.
                                                                                                                                                       Gaps
                                                                                                                                                                                                             Nakahara K, Tamaki I, Takahashi T;
                                                                                                                     Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine anti-Fas antibody HFE7A light chain protein.
                                                                                                                  100.0%; Score 205; DB 21; 39.7%; Pred. No. 1.2e-05; ive 47; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example reference 4; Page 104; 263pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                       AAW90898 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99EP-0307711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0276882
                                                                                                                                                                                                                                                              61 XXXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serizawa N, Haruyama H,
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N-PSDB; AAA11547.
                                                                                                                                      Similarity
                                                               238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                 Sequence
                                                                                                                   Query Match
                                                                                                                                      Best Local
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                                                                                                                                                       Matches
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antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibitation of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
ersus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
anuliple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
E. C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a murine anti-Fas monoclonal antibody HFE7A light chain described in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; derti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 205; DB 21;
39.7%; Pred. No. 1.2e-05;
iive 47; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
c apoptosis in cells with a normal system, by inhibiting binding between
c apoptosis in cells with a normal system, by inhibiting binding between
c anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
c mildiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
c antiarterioscleroric, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
c apoptosis by binding to cell surface Fas or inhibit it by competitive
c apoptosis by binding to cell surface Fas or inhibit it by competitive
c apoptosis by binding to cell surface Fas or inhibit it by competitive
c apoptosis by binding to cell surface Fas or inhibit it by competitive
c diseases associated with the Fas/Fas ligand system, especially systemic
c lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
c versus host disease, Slorgederma, Goodpasture syndrome, Crohn's
c disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
caliental Addison's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
c ardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
c (B, C or D) or alcoholic), and transplant rejectively induce it in abnormal
c cells. They bind to both human and murine Fas, so can be evaluated in
c murine disease models. (I) act on the active site of Fas, i.e. they minic
c the native ligand, do not induce liver disease, and have reduced risk of
c inducing a human anti-murine antibody response. This sequence represents
c humanised anti-reas antibody HEFA light chain HH type which is used in
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                                                                     New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                                                            Example reference 14; Page 114-115; 263pp; English.
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7; Mismatches
                                                                                                                        cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90923 standard; Protein; 238 AA.
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39.7%; P
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Best Local Similarity 39.7%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2000 (first entry)
WPI; 2000-258930/23.
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                         N-PSDB; AAA11562
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cells with an abnormal Fas/Fas

co apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-memic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

confiscases associated with the Fas/Fas ligand system, especially systemic

diseases associated with the Fas/Fas ligand system, especially systemic

clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Sjorgem's syndrome, pernicious or hypoplastic

cupus erythematosus, Hashimoto disease, theumatoid arthritis, graft

versus host disease, Sjorgem's syndrome, pernicious or hypoplastic

cupus erythematosus, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

cardiomyopathy, glomerulomephritis, hepatitis (fulminant, chronic, viral

cells. They bind to both human and murine fises, i.e. they mimic

che native ligand, do not induce liver disease, and have reduced risk of

the native ligand, do not induce liver disease, and have reduced risk of

inducing a human anti-murine antibody response. This sequence represents

ca humanised anti-Fasa antibody HERFA light chain HM type which is used in

cupus erythemative light on the normal contains of the nethod described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Mismatches
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98JP-0276882.
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Best Local Similarity 39.7%
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         2000-258930/23.
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                                                                                                                                                                         29-SEP-1999;
                                                                                                                                                                                                                    30-SEP-1998;
                                                                                                                                                                                                                                         30-SEP-1998;
                                                                                    EP990663-A2
                                                                                                                             05-APR-2000
                                         Synthetic.
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completed: August 14, 2002, 15:15:34 ne: 832 sec

Search com Job time:

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2991464/10

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:17:02; Search time 82.88 Seconds (without alignments) 22.987 Million cell updates/sec

5_G_6_G_7 205 Title: Perfect score:

Sedneuce:

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

231628 seqs, 24425594 residues Searched:

231628 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*

APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ANDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia

COUNTRY: USA

ZIP: 19406-0939

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 73, Appl	73,	58,	58,	2, 4		9	9	æ	٦	51,	14,	18,	7	14,	14,	~	24,	Sequence 24, Appl	6, 2	9	9	10,	10,	10,	Sequence 13, Appl	ø , 6
SUMMARIES	ID	US-08-483-636-73	US-08-483-632-73	-483	US-08-483-632-58	-483	US-08-483-632-2	-466	-466-	US-08-491-845-8	US-08-491-845-16	US-08-513-968-51	US-08-579-378A-14	US-08-579-378A-18	PCT-US96-13152-2	US-08-483-636-14	US-08-483-632-14	US-08-111-080-24	US-08-211-980-24	PCT-US93-07967-24	US-08-887-352B-6	US-09-109-207C-6	us-09-296-005-6	US-08-887-352B-10	US-09-109-207C-10	US-09-296-005-10	-3	US-08-466-151-9
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æ	Query	9.96	9.96	9.96	9.96	9.96	9.96	96.1	96.1	96.1	96.1	96.1	96.1	96.1	96.1	95.1	95.1	868	86.8	869.8	88.8	88.8	88.8	88.8	88.8	88.8	88.8	88.8
	Score	198	198	198	198	198	198	197	197	197	197	197	197	197	197	195	195	184	184	184	182	182	182	182	182	182	182	182
	Result No.	1	7	3	4	2	9	7	œ		10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-28P-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGEN: 1NFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELEPHONE: (215) 270-5090
TELEFRA: (215) 270-5090

28	182	88.8	218	4	US-09-109-207C-13	13,
29	182	œ	218	4	US-09-296-005-13	13,
30	182	8	218	4	US-08-466-163B-9	ď
31	178	ė.	111	7	US-08-887-352B-5	'n
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36	178	ė,	114	~	US-08-887-352B-9	σ,
37	175	ď.	114	4	US-09-109-207C-9	σÌ
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39	165	。	239	7	US-08-553-497A-18	18,
40	159	۲.	114	~	US-08-887-352B-8	æ
41	159	7.	218	4	US-09-282-505-1	1,
42	159	7.	218	4	-09-054-	٦,
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44	156		114	4	US-09-296-005-8	8, 8
45	156	•	218	7	US-08-887-352B-15	15,
					ALIGNMENTS	
RESULT	1					
US-08-483-636-73; Sequence 73, A	-636-7	-08-483-636-73 Sequence 73, Application US/08483636 Datent No. 5914110	ion US,	708	483636	
	NERAL INFOR	GENERAL INFORMATION:	;			
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0; Gaps
                                              24 KASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLESGIPSRFSGSGGGTDFTFTISSLQ 83
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                                                                                                                                                                                                                                                             US-08-483-636-58
Sequence 58, Application US/08483636
Sequence 58, Application US/08483636
Sequence 58, Application US/08483636
Setent No. 2514110
SENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treellectual Property CARETT: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.6%; Score 198; DB 2; 38.5%; Pred. No. 5.1e-08; tive 47; Mismatches 1
  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 14-00T-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-00T-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US/94/10308
FILING DATE: 07-5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sutton, Jeffrey A.
REGISTATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPHONE: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            84 PEDIATYYCQQSNEDPPT 101
    Conservative
                                                                                                                                     61 XXXXXXXXQQSNEDPRT 78
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amino acid
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Matches 30; Conservative
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                                                                                     ; Score 198; DB 2; Length 111;
; Pred. No. 3.1e-08;
47; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATR:

APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treepres. P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198; DB 2;
Pred. No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07.5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73, Application US/08483632 Patent No. 5928904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                       96.6%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.6%;
38.5%;
                                                                                                                                                                                                                                                                                             61 XXXXXXXXQQSNEDPRT 78
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                                                                                                              Best Local Similarity 38.59
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
; MOLECULE TYPE:
US-08-483-636-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-08-483-632-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-632-73
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                                                                                         Query Match
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44 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 132;
                                      APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II.4 Antibodies Useful in TITLE OF INVENTION: Treatment of II.4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant LL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of LL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 198; DB 2;
; Pred. No. 5.2e-08;
47; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07.SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-483-632-2
; Sequence 2, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPy disk
COMPUTER: IBM PC COMPAILble
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38.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
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Best Local Similarity 38.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-483-636-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                          GENERAL INFORMATION:
    Patent No. 5914110
                                                                                                                                                                                                                                                                                                    PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 131;
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-0939
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treflectual Property Carberre P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.6%; Score 198; DB 2; 38.5%; Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
ATTORNEY AGENT INFORMATION:
NAME: SULLON, JEFFREY A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  Sequence 58, Application US/08483632 Patent No. 5928904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08483636
AEDVAVYYCQQSNEDPPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-483-632-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Kir
STATE: PI
COUNTRY:
                                                                                       RESULT 4
US-08-483-632-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-483-636-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                     셤
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Gaps

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24 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.1%; Score 197; DB 3;
nilarity 38.5%; Pred. No. 3.3e-08;
Conservative 47; Mismatches 1.
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                            CURREMY ARPLICATION DATA:

APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFTCATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/466163
FILING DATE: 15-MRA-1995
APPLICATION NUMBER: 08/185899
FILING DATE: 15-MRA-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/44768
FILING DATE: 07/HAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-NGC-1991
ATTONEY/AGENT INFORMATION:
NAME: SVODGGA, CTAIJ G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFIEROMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                    SYSTEM: PC-DOS/MS-DOS WinPatin (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 106 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 EEDAATYYCQQSNEDPFT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-466-163B-6
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LENGTH: 106
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                                                                                                                                                                         COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 6, Application US/08466151
; Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 132 amino acids
amino acid
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NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MAEDA=5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-513-968-51; Sequence 51, Application US/08513968; Patent No. 6114143; Patent No. 6114143; GENERAL INFORMATION:
                                                                                                                                                       Sequence 16, Application US/08491845 Patent No. 5773247
                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                        84 EEDGATYYCQQSNEDPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 PEDIATYYCQQSNEDPWT 101
                    61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 XXXXXXXXQQSNEDPRT 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-491-845-16
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20004
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                    RESULT 10
US-08-491-845-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                         qq
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                                                                                                                                                         1 KASQSVDYDGDSYMNXXXXXXXXXXXXXASNLESXXXXXXXXXXXXXXXXXXXXX
                                                                                                                    ö
                                                                               Length 106;
                                                                           96.1%; Score 197; DB 4; Length 10
38.5%; Pred. No. 3.3e-08;
.ive 47; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PRCCESS FOR PREPARING THE SAME
MUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPEN Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.1%; Score 197; DB 1; 38.5%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MAEDA=5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08491845
Patent No. 5773247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MAEDA, Hiroaki
APPLICANT: KIMACHI, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         84 EEDAATYYCQQSNEDPFT 101
                                                                                                                                                                                                                                  61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 111 amino acids TYPE: amino acid
                                                                           Query Match 96.18
Best Local Similarity 38.58
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-491-845-8
; ORGANISM: Mus musculus US-08-466-163B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-491-845-8
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1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.1%; Score 197; DB 1; Length 111; 38.5%; Pred. No. 3.7e-08;
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, KIyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PRCCESS FOR PREPARING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                 Erowdy and Neimark
419 Seventh Street N.W. Ste. 300
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44 KASQSVDYDGDSYMNWYQQKPGQPPKILIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
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Sequence 18, Application US/08579378A
Sequence 18, Application US/08579378A
Sequence 18, Application US/08579378A
SEQUENCE CO, Man Sung
TITLE OF INVERVION: Humanized Antibodies Reactive with
TITLE OF INVERVION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew One MarketPlaza, Steuart Tower, Suite 2000
                  ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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96.1%; Score 197; DB 4;
Best Local Similarity 38.5%; Pred. No. 6.2e-08;
Matches 30; Conservative 47; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11823-002220
                                                                                                                                                                         ACCORDING TATELLIAN NUMBER: US/08/579,378A
PILING DATE: 27-DEC-1995
CLASSIFICATION: 244
RUCA REPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 11-DEC-1992
PRIOR APPLICATION NUMBER: E95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: E95112895.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
ANAME: 11-DEC-1995
                                                                                                                                                                омыек: US/08/579,378A
27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Liebescheutz, Joe O. REGISTRATION NUMBER: 37,505 REFERENCE/DOCKET NUMBER: 118 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAN. 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 XXXXXXXXQQSNEDPRT 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One MarketPl
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %308-579-378A-14

Sequence 14, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L. Selectin

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew STREET: One Marketlaza, Steuart Tower, Suite 2000 STRY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FLING DATE: 11-SEP-1995
CLASSIFICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25.618
                                                                                                                                                                              TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
                                                                                         OSATOMI, Kiyoshi
KIMACHI, Kazuhiko
HIGUCHI, Hirofumi
TOKIYOSHI, Sachio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: ED.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                        MAKIZUMI, Keiichi
SHIOSAKI, Kouichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 PEDIATYYCQOSNEDPWT 105
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amino acid
3X: linear
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EDA, Yasuyuki
MAEDA, Hiroak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-513-968-51
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                      STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                   20004
                                                                                                                                                                                                                                                         ADDRESSEE:
                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                     APPLICATION NUMBER: BP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BEER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEBHONE: (212) 688-9200
TELEBHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.1%; Score 197; DB 5; 38.5%; Pred. No. 2.9e-07; iive 47; Mismatches 1
       17-Aug-95
JMBER: EP 95 114 969.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCI/US/94/10308
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136/783
FILING DATE: 14-OCT-1993
PROR APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08483636; Patent No. 5914110; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 PEDFATYYCQQSNEDPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.1%
Best Local Similarity 38.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-2
                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-483-636-14
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GENERAL INFORMATION:
    APPLICANT: Martin, Ulrich, et al.
    TITLE OF INVENTION: Atti-selectin antibodies for prevention of multiple organ fai
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Attn: Norman D. Hanson
    STREET: 805 Third Avenue
    CITY: New York
    STATE: New York
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.1%; Score 197; DB 4; Length 13
38.5%; Pred. No. 6.2e-08;
ive 47; Mismatches 1; Indels
                                                          FILING DATE: A'DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATORNEY/ACENT INFORMATION:
NAME: Libebscheutz, Joo O.
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE ATORNEY: 415-326-24400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
APPLICATION NUMBER: EP 95 112 895.8
APPLICATION NUMBER: EP 95 112 895.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 PEDFATYYCQOSNEDPWT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 XXXXXXXXQQSNEDPRT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.55
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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PCT-US96-13152-2
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5_9_6_9_7.rpr

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:18:57 ; Search time 108.64 Seconds (without alignments) 68.989 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

5_G_6_G_7 205_ABGQSVDVDGDSYMNXXXXX.....XXXXXXXXXXXXQQSNEDPRT 78

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq kappa chain V r	kappa cha	kappa		kappa	kappa			kappa chain	Ig kappa chain V-J				1.3			kappa	kappa	light chain					kappa chain	light		kappa	chain	
SUMMARIES	O.	KVMS83	KVMS43	KVMS69	A38601	KVMS08	S42193	S19971	PH1226	KVMSC1	996608	KVMS10	S19976	S19972	D45722	S26344	KVMS37	S26343	KVMSM6	B49442	S63596	KVMS84	S09965	KVMS32	РН0093	PH1079	PL0081	S06731	KVMS80	KVMS54
	DB	1	7	-	7	-	~	7	~	П	7	Т	~	7	C	~	Н	7	Н	7	7	_	7	П	7	7	~	7	-	_
	Length	111	111	111	93	111	81	112	131	111	111	110	112	112	111	107	111	107	131	96	115	111	111	132	109	102	111	120	111	108
ď	ery	96.6	96.1	96.1	94.1	94.1	93.2	92.7	ć.	÷	7	84.1	œ.	φ.	9.9/	υ.	2.	ъ.	73.7	ä	ä	9	٠.	٠.	S.	4	64.9	4	64.4	63.4
	Score	198	197	197	193	193	191	190	190	187	179	172.5	172	162	157	155	155	154	151	149	147	137	136	136	135	133	133	133	132	130
	Result No.	-	7	m	4	'n	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT KVMS43

Name of the control o

kappa chain	kappa chain	kappa chain	kappa chain	light chain	Ig kappa chain V-J	kappa chain	kappa chain	kappa chain	kappa	kappa			Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r
KVMS75	806608	E53285	506732	PH1076	696608	A56169	KVMS40	S37202	S45715	S40331	KVMS85	JC5810	KVMS50	S68241	B49047
Т	7	~	7	7	7	7	Н	ď	~	7	٦	~		7	7
111	111	111	120	102	111	210	111	111	112	123	111	218	111	218	108
63.4	63.4	63.4	63.4	62.8	62.9	62.8	62.0	62.0	62.0	62.0	61.0	60.5	0.09	59.0	58.5
130	130	130	130	129	129	129	127	127	127	127	125	124	123	121	120
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT KVMS83	3 1
Ig ka	Ig kappa chain V region (PC7183) – mouse
C;Spe C;Dat	C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Acc	C; Accession: B01937; A01937
R; Wei	R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
A:Tit	Nature 2/0, 782-790, 12/8 ArTitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Ref	A;Reference number: A93204; MUID:79073152
A; Acc	ession: B01937
A; Mol	A;Molecule type: protein
C; Com	plex: An immunoqlobulin heterotetramer subunit consists of two identical light (
hain	hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C; Sup	C;Superfamily: immunoglobulin V region; immunoglobulin homology
C; Key	C;Keywords: heterotetramer; immunoglobulin
F;16-	94/Domain: immunoglobulin homology <imm></imm>
F; 23-	F;23-92/Disulfide bonds: #status predicted
ono	Ouery Match 96.6%; Score 198; DB 1; Length 111;
Bes	Best Local Similarity 38.5%; Pred. No. 2.2e-09; Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;
QY	1 KASQSYDYDGDSYMNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
qq	24 KASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
Qy	61 XXXXXXXXXQQSNEDPRT 78
ΩD	::::::: 84 EEDAATYYCQQSNEDPLT 101

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Ig kappa chain V region (PC6308) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Accession: C01937; A01937
Nature 276, 785-790, 1978
N; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
N; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUD: 79073152
A; Accession: C01937
A; Molecule type: protein
A; Residues: 1-111 < WEI>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (complex: An immunoglobulin V region: immunoglobulin homology
C; Superfamily: immunoglobulin V region: immunoglobulin
F; 16-94/Domain: immunoglobulin homology < iMM>
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mis misculus (house mouse)
C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C; Rccession: A36601
A; Title: Common structural features among monoclonal antibodies binding the same anti
A; Title: Common structural features among monoclonal antibodies binding the same anti
A; Reference number: A36601; MUD:91115823
A; Reference number: A36601; MUD:91115823
A; Residues: 1-93 <GOS>
A; Residues: 1-93 <GOS>
A; Residues: 1-93 <GOS
A; Residues: 1-93 <GOS
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                         Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%; Score 193; DB 2; Lularity 37.2%; Pred. No. 5.4e-09; Conservative 47; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.1%; Score 193; DB 1; L. Best Local Similarity 37.2%; Pred. No. 7.1e-09; Matches 29; Conservative 47; Mismatches 2;
                                                                                         Score 197; DB 1;
Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region (1G3) - mouse (fragment)
                                                                                                                                                          47; Mismatches
F;23-92/Disulfide bonds: #status predicted
                                                                                            96.1%;
38.5%;
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                                                                                                                                                                                                                                                                                                                                                                61 XXXXXXXXQQSNEDPRT 78
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                                                                                                                                                                Conservative
                                                                                            Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local Similarity
Matches 29; Conserv
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A; Note: V-kappa-21E; anti-collagen
C; Complex: An immunoglobulin heterotramer subunit consists of two identical light (kappa-16: an immunoglobulin heterotramer subunit consists of two identical light (kappa disulfide bonds: In some cases, such as 1gA and 1gM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology < IMM>
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;16-94/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ig kappa chain V region (PC7769) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Sate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C; Accession: E01937, A01937
R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUID:79073152
A; Motecule type: protein
A; Residues: 1-111 < WEI>
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                       Residues: 10-99 <MOJ>
:Residues: 10-99 <MOJ>
:Cross-references: EMBL:225444; NID:g407832; PIDN:CAA80931.1; PID:g407833; Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                       A;Cross-references: EMBL:225458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42190
                                                                                                                                                                                                                                                                                                                                                                                     A;Cross.references: EMBL:225450; NID:g407838; PIDN:CAA80937.1; PID:g407839 A;Note: V-kappa-21E; anti-collagen A;Note: V-kappa-21E; anti-collagen A;Accession: $42189 A;Accession: $42189 A;Accession: $4299 A;Accession: $4289 A;Residues: 15-99 AMOA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 12-99 <MOZ>
A; Cross-references: EMBL:225446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A; Note: V-Kappa-21E; anti-collagen
A; Note: V-Kappa-21E; anti-collagen
A; Molecule type: DNA
A; Residues: 10-99 <MOY>
A; Cross-references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A; Note: V-Kappa-21E; anti-collagen
A; Accession: S42192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEDAATYYCQQSNEDPFT 101
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nes 30; Conserv
                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 13-99 <MOF>
                                                                                                                                                          Molecule type: DNA; Residues: 12-99 < MOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 10-99 <MOO>
                                                                                                                              A; Accession: S42194
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Best Local S
Matches 30
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R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; I Gene 121, 271-278, 1992
Gene 121, 271-278, 1992
A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A;Reference number: PH1224; MUID:93077041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A) Note: this mouse sequence was hybridized and fused with a human constant region gen
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E;1-20.70main: signal sequence #status predicted <SIG>
F;21-30.70main: aignal sequence #status predicted <MAT>
F;36-114/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related A;Reference number: A93822; MUID:79012520
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A; Residues: 1-111 <MCK>
A; Residues: 1-111 <MCK>
C; Comment: This chain was isolated from a myeloma protein.
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
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                                                                                                                                                                                                                                                                                   Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 KASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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   24 KASQSLDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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Pred. No. 1.8e-08;
9; Mismatches 1;
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Pred. No. 2.9e-08;
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1 Similarity 35.9%;
28; Conservative 4
                                                                                               EEDAATYYCQQSSEDPPT 101
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Best Local Similarity
Matches 28; Conserv
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Best Local Similarity
Matches 28; Conserv
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A; Molecule type: mRNA
A; Residues: 1-131 <WEI>
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R;MO, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec A;Reference number: $42176; MUID:94009207
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:225456; NID:g407846; PIDN:CAA80943.1; PID:g407847 A;Cross-references: EMBL:225456; NID:g407847 ED: A;Note: Inh authors translated the codon GTT for residue 36 as Ala C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX
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35.9%; Pred. No. 1.5e-08;
ive 49; Mismatches 1;
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; Pred. No. 7e-09;
47; Mismatches
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                                                                                                                          XXXXXXXXQQSNEDPRT 78
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Best Local Similarity 36.89
Matches 28; Conservative
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Best Local Similarity
Matches 28; Conserv
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A; Residues: 1-81 <MOJ>
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C;Accession: D45722
R;Simpson, J-A.; Chow, J-C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A;Reference number: A45722; MUID:93100833
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep_1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
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C;Accession: S1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Reference number: S19963
A;Status: preliminary
A;Residues: 1-112 <WEI>
Species: Mus musculus (house mouse)
Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA4621.1; PID:g52299 C.S. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:l6-94/Domain: immunoglobulin homology <IMM>
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                                                                                 Е.Р.
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                                            C. Accession: S1976
R. Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, Submitted to the EMEL Data Library, March 1992
A. Description: Structural characterization of CD4 mAb.
A. Reference number: S19963
A. Accession: S19976
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-112 <WEI>
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Pred. No. 9.4e-07;
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A; Residues: 1-110 
A; Residues: 1-110 
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology 
F; 16-94/Domain: immunoglobulin homology 
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                    Ig kappa chain V-J region (1E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 809966
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MUID: 90269328
A;Accession: 809966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231 Cs.Superfamily: immunoplobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:16-94/Domain: immunoglobulin homology <IMM>
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39.7%; Pred. No. 1.8e-07;
Live 44; Mismatches 3; Indels
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34.6%; Pred. No. 8.2e-07;
iive 48; Mismatches 2;
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Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 326344
A;Title: Antibodies that are specific for a single amino acid interchange in a protein (A;Reference number: $26309; MuID:91341421
A;Title: Antibodies that are specific for a single amino acid interchange in a protein (A;Reference number: $26309; MuID:91341421
A;Accession: $2634
A;Accession: $2634
A;Accession: $2634
A;Accession: $26309; MID:952336; PIDN:CAA41919.1; PID:91334074
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin homology <IMM>
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               A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Rolecule type: nucleic acid A;Rolecule type: nucleic acid A;Rolecule type: nucleic acid A;Note: sequence extracted from NCBI backbone (NCBIP:120592) C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                   Query Match 76.6%; Score 157; DB 2; Length 111; Best Local Similarity 28.2%; Pred. No. 3e-05; Matches 22; Conservative 52; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
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Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01666 mus musculu	P01665 mus musculu	P01669 mus musculu	P01667 mus musculu	P01664 mus musculu	P01668 mus musculu	P01660 mus musculu	P01662 mus musculu	mus	mus	P01670 mus musculu	P01659 mus musculu	Snu	P01656 mus musculu	mus	P01674 mus musculu	шns	mus	P01672 mus musculu	P01673 mus musculu	P03977 mus musculu	homo	homo	homo	homo	рошо	homo	homo	шns	P01648 mus musculu	P01645 mus musculu	2 homo	P06310 homo sapien
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24 KASQSVDYDGDSYMNWYQQKPGQPPKVLIFAASNLESGIPARFSGSGSGTDFTLNIHPVE 83
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE-79073152; PubMed-103003;
Medjert M., Gatmaltan L., Loh E., Schilling J., Hood L.E.;
Weigert M., Gatmaltan L., Information may produce immunoglobulin
Alvarsity.";
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                        COMPLEMENTARITY - DETERMINING - 2. FRAMEWORK - 3.
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COMPLERENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
  COMPLEMENTARITY - DETERMINING-1.
                                               COMPLEMENTARITY - DETERMINING - 3.
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                                                                                              12011 MW; 6FAA345279356829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12071 MW; 7A4ADE4D6C256D29 CRC64;
                                                                                                                    96.1%; Score 197; DB 1; L6
38.5%; Pred. No. 8.1e-08;
                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 6308.
                                                           FRAMEWORK-4.
BY SIMILARITY.
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BY SIMILARI
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PIR; CO1937; KVMSO8.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV: 1.
Immunoglobulin V region.
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Best Local Similarity 38.5%
Matches 30; Conservative
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P01667;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7043.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                      MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Rood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region PC 7769.
Mus musculus (Mouse).
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HSSP; P01789; IMCP.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam: PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
-DOMAIN.
                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Nature 276:785-790(1978).
                                                                                                                                           diversity.";
Nature 276:785-790(1978).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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HSSP; P01789; 1MCP.
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Best Local Similarity
Matches 30; Conserv
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P01669;
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                                                                                                                                                           McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
HSSP; PO1789; IMCP.
InterPro; IPR003506; Ig_MC.
InterPro; IPR003596; Ig_V.
SMART: SM00406; Ig; I.
Immunoglobulin V region.
DOMAIN.
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                            FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                           91.2%; Score 187; DB 1; Length 111; 35.9%; Pred. No. 5.8e-07; ive 48; Mismatches 2; Indels
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                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region CBPC 101.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7210.
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Nature 276:785-790(1978).
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111 AA;
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                                 KV3L_MOUSE
P01664;
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P01668;
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KV3P_MOUSE
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MEDLINE=7901250; PubMed=99744;

MECHANISME OF 1201250; PubMed=99744;

MCKAANISMS of Antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Trelated mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

PIR, A01934; KWMS37.

R HSSP, P01789; IMCP.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003006; Ig_WC.

R FMART; SM00407; ig; 1.

FMMUNOGlobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                84.1%; Score 172.5; DB 1; Length 110; 34.6%; Pred. No. 9.7e-06; ive 48; Mismatches 2; Indels 1
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                                                                                                                                                                                                                                                                                                                          69F1A5CE886B1249 CRC64;
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
May Rappa chain V-III region PC 3741/TEPC 111.
Mus musculus (Mouse).
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PIR; D01937; KVMS10.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig'. Ig_NARRT; SM04406; IGv; I
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Best Local Similarity 34.69
Matches 27; Conservative
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SEQUENCE OF 1-35.
MEDLINE-78235887; PubMed-98179;
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PIR; A01935; KVMSM6.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
84 ADDAATYYCQQNNEDPYT 101
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Best Local Similarity 26.9%
Matches 21; Conservative
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MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                       Gaps
                                                                                                                            24 RASESVDSYGNSFWHWYQQKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                             KV3J_MOUSE STANDARD; PRT; 111 AA.
P01663;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Muss musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 276:785-790(1978).
-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
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MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                            ; Score 155; DB 1; Length 111;
; Pred. No. 0.00031;
52; Mismatches 4; Indels
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FRAMEWORK-2.
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                         EC46C9D259213BE4 CRC64;
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BY SIMILARITY.
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23 CON

53 FR2

60 CON

101 CON

111 FR2

12041 MW; I
                         12099 MW;
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HSSP; P01789; IMCP.
InterPro; IPR0013006; Ig_MHC.
InterPro; IPR0013506; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                            ch 75.6%;
1 Similarity 28.2%;
22; Conservative 5.
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111 AA;
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                                                                                                                                                                 Mus musculus (Mouse).

Was musculus (Mouse).

Wasaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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COMPLEMENTARITY - DETERMINING - 2.
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COMPLEMENTARITY-DETERMINING-3.
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12005 MW; 39D87619313453CB CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 4050.
111 AA.
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BY SIMILARI
PRT;
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Gaps

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McKean D.J., Potter M., Hood L.E.;

Landle State Mills and McKean Sequence of Inferences.";

Blochemistry 12:760-771(1973).

R PIR, A01933, KWAS32.

R HSSP, P01607; JREI.

R InterPro; IPR003066; Ig_MC.

R Pfam, PF00047; ig, 1.

R SMART; SW00406; ig, 1.

M Immunoglobulin V region.

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1 23 FRAMEWORK-1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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illarity 19.2%; Pred. No. 0.013;
Conservative 58; Mismatches 5; Indels
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COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region TEPC 124.
Mus musculus (Mouse).
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InterPro; IPR003596; Ig_v.
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                       SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Matches 20;
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KV3G_MOUSE
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MEDLINE=79012520; PubMed=99744;

MEChanisms of antibody diversity:

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MEDLINE-73140225; PubMed-4691517;
McKaan D.'., Potter M., Hood L.E.;
Mouse inmunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-III REGION MOPC 63.
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precursors: implications on the organization and controlled
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6684.
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                                 expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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PIR; A01938; KVMS84.
HSSP; P01789; 1MCP.
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131 AA;
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P01670;
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MEDLINE-79073152; PubMed=103003;
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity 25.6'
Matches 20; Conservative
                               STANDARD;
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 RESULT 14
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MEDLINE-73140224; PubMed-4120629;
McKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
24 RASZSVNWYGNSFMZWYZZKPGZPPKLLIYRASNLZSGIPARFSGSGSRTBFTLTIBPVZ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXX 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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19.2%; Pred. No. 0.018;
iive 58; Mismatches 5; Indels
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                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region MOPC 321 precursor.
                                                                                                                             132 AA.
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FRAMEWORK-1
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                                                                                                                                                                                                                                                                                                                                                                            expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain.";
Biochemistry 12:749-759(1973).
                                                 84 ABDVATYFCZZSBZAPWT 101
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                            61 XXXXXXXXQQSNEDPRT 78
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SMART; SM00406; IGv; 1.
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Best Local Similarity
Matches 15; Conserv
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SEQUENCE OF 1-37.
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P01658;
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-!- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL..
PIR; A01930; KVMS80.
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sciurognathi; Muridae; Murinae; Mus
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Gray W.R., Dreyer W.J., Hood L.E.;
"Mechanism of antibody synthesis: size differences between mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Kappa cnains.; | Science 155:465-467(1967). | Colones Protein. | Science 155:465-467(1967). | Colones Protein. | Colones Protein. | First. A01930; KVMS80. | Riss. Pol 789; ImcP. | 
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25.6%; Pred. No. 0.016;
ive 50; Mismatches
                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region MOPC 70.
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 2880/PC 1229.
111 AA.
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DR HSSP: P01789; 1MCP.

DR InterPro; IPR003006; Ig_MC.

DR InterPro; IPR003506; Ig_V.

DR InterPro; IPR003506; Ig_V.

DR InterPro; IPR003506; Ig_V.

DR SMART; SM00406; Ig_V.

KW Immunoglobulin V region.

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 39 53 FRAMEWORK-2.

FT DOMAIN 61 92 FRAMEWORK-3.

FT DOMAIN 61 92 FRAMEWORK-1.

FT DOMAIN 62 92 FRAMEWOR
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Search completed: August 14, 2002, 15:23:12 Job time: 685 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:22:12 ; Search time 187.61 Seconds (without alignments) 71.924 Million cell updates/sec

Perfect score:

5_G_6_G_7 205 1 KASQSVDYDGDSYMNXXXXX.....XXXXXXXXXXXQQSNEDPRT Sequence:

BLOSUM62DX Scoring table:

Searched:

Gapop 10.0 , Gapext 0.5

562222 Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database

sp_archea:* sp_bacteria:*

sp_invertebrate:*
sp_mammal:* sp_organelle:*
sp_phage:* sp_fungi:* sp_human:* sp_mhc:*

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_bacteriap:*
sp_archeap:* sp_rodent:* sp_rvirus:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ulusum sum O81:60:	0920e9 masculu	O96sa9 homo sapien	09ul77 homo sapien	Q9ul81 homo sapien	Q9ul70 homo sapien	Q9u180 homo sapien	Q96jm2 homo sapien	O09004 mus musculu	Q9pmz3 campylobact	Q9fvq1 arabidopsis	Oganag musculu	000538 homo sapien	Q9u165 homo sapien	O9h1b6 homo sapien	Q9j176 mus musculu
	ID	08.11.80	0920E9	Q96SA9	Q9UL77	Q9UL81	Q9UL70	09UL80	096лм2	008004	Q9PMZ3	Q9FVQ1	690060	000538	Q9UL65	Q9H1B6	Q9JL76
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æ	Query Match	65.9	63.4	55.1	55.1	53.7	52.7	51.0	50.2	49.3	49.3	49.3	49.3	49.3	49.3	49.3	49.0
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Gaps

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0.11; has 7; Indels

1 KASQSVDYDGDSYMNXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXX 60

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Query Match 65.9%; Score 135; DB 11; Length 103; Best Local Similarity 24.4%; Pred. No. 0.11; Matches 19; Conservative 52; Mismatches 7; Indels

007324 staphylococ govms2 drosophila P72573 streptococc P7257 streptococc goput o staphylococ goput o gopu	099345 human immun 099644 talpa altai 090491 human immun 090405 human immun
2 007324 5 09VMS2 2 P72503 2 P72503 16 09PKMS 6 099UT0 6 099UT0 10 09LLC8 10 09LLC8 10 09LLC8 11 09LL78 11 09LL78 11 09S57 11 09S57 12 09A85 5 09V828 11 09A85 5 09V828 7 095513 7 095514	15 Q93345 15 Q94345 6 Q9BFQ4 15 Q904G1 15 Q904N5
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ALIGNMENTS

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XX STRAINBALBACK,
XX MEDLINE=20448942; PubMed=10992488;
XX MEDLINE=20448942; PubMed=10992488;
XX MEDLINE=20448942; PubMed=10992488;
XX MAINIEL S., Liao L., Cunningham M.W., Diamond B.;
XX T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
XX Interpros F80362. INTL.
XX HSSP; P80362; IMTL.
XX HSSP; P80362; IMTL.
XX HSSP; P80362; IMTL.
XX HSSP; P80362; IG_V.
XX InterPro; IPR003006; IG_V.
XX InterPro; IPR003096; IG_V.
XX SMART; SM00406; IGV; 1.
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XX 11224 MW; EC87D653DB3AB21 CRC64;
                                                                                                                                                              Eukaryota...
Eukaryota., Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthazoa; Modentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                103 AA.
                                 PRT;
                                PRELIMINARY;
                                                                                                                                  (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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09JL80;
RESULT
Q9JL80
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24 RASQSI----SSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQ 79
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Wu Z., C., C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.1%; Score 113; DB 4; Length 108; ilarity 20.8%; Pred. No. 7.8; Conservative 52; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNGCLOBULIN LIGHT CHAIN VARIABLE REGION
                                   Indels
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EMBL; AF035037; AADS6273.1; -.
HSSP; P01607; 1REI.
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1 Similarity 20.8%; Pred. No. 7.6; 15; Conservative 52; Mismatches
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   Best Local Similarity
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EMBL: AF307935; AAL09419.1; -
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16 RASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVE 75
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPPROCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68765.1;
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                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
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11520 MW;
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107 AA;
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                           Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
Wu X., Liu B., Van der Merwe P.L., Kalls N.N., berney _{^{2}.^{2}.^{2}} Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                 Query Match 53.7%; Score 110; DB 4; Length 107; Best Local Similarity 19.4%; Pred. No. 13; Matches 14; Conservative 53; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
(FRAGMENT).
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NON_TER 107 107
SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
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108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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EMBL, AF035044; AAD56280.1; -.
HSSP, P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                       Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD35033, AAD56269.1; -.
INTESP: POL607; 1REI.
INTERPRO; 1PR003006; Ig_MHC.
INTERPRO; 1PR003596; Ig_N.
INTERPRO; 1PR0047; ig; 1.
SMART; SM00406; IGV; 1.
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MEDLINE=98277139; PubMed=9614934;
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Best Local Similarity 17.9%
Matches 14; Conservative
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SMART; SM00406; IGv; 1.
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80 AEDFATYYCQQS 91
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"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro.";
DNA Res. 8:85-95(2001).
EMBL. ABOS8706; BAB47432.1; -.
SEQUENCE 1299 AA; 148675 MW; 69FFECB5868186DD CRC64;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035034; AAD56270.1; -.
HSSP; P80362; IWTL.
114 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.0%; Score 104.5; 116.9%; Pred. No. 43; ive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1299 AA
PRT;
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TISSUE-BRAIN;
MEDLINE-21245130; PubMed=11347906;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 AA; 12775 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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KIAA1803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 EAEDVGVYYCMQGTHWP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 51.0%
Best Local Similarity 16.9%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 XXXXXXXXXQQSNEDP 76
PRELIMINARY;
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                                                                                                                                                                                         Homo sapiens (Human).
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Q9FVQ1;
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Q9FVQ1
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0
                                                      88 RNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMISYFLRSSSVLGGRM 147
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         1 KASQSVDYDGDSYMNXXXXXXXXXXXXXXAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                       are
                                                                                                                                                                                                                                                                                      MEDLINE-98001089; PubMed-9341881;
A Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
A Gagarcrantz J., Blennow E., Mehlin H., Dumanski J.;
Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
The germinal centre kinase gene and a novel CDC25-like gene are
I located in the vicinity of the PYGM gene on 11q13.";
Hum. Genet. 100:611-619(1997).
I-- SIMILARITY: TO OTHER EP-HAND CALCIUM BINDING PROTEINS.
REMBL: Y12339; CAA73008.1; -.
HSSP; P28867; 1PTQ.
RGD; MGI:1333849; Rasgrp2.
RICEPPO; IPRO02219; DAG_PE-bind.
RICEPPO; IPRO02219; DAG_PE-bind.
Remi: PF00036; efhand; 2.
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 Length 1299;
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                      11; Indels
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                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN CJ1306C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.3%; Score 101; DB 11;
12.9%; Pred. No. 4.8e+02;
tive 55; Mismatches 6;
50.2%; Score 103; DB 4; 17.3%; Pred. No. 9.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                    51; Mismatches
                                                                                                                                                                               01-JUL-1997 (TrEMBLEEL 04, Created)
01-JUL-1997 (TREMBLEEL 04, Last sequenc
01-DEC-2001 (TrEMBLEEL: 19, Last annotat
F25B3.3 KINASE LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00109; C1; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
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                                                                                               1229 HGMALNDTKQVSREE 1243
                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium-binding; Kinase.
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                                                                                    61 XXXXXXXXQQSNED 75
           Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE
Query Match
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                      Matches
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009004
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C. STRAIN=CV. COLUMBIA;
A. Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
In X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maitl R., Ronning C.M., Koo H., Fujii C.Y., Ulterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
T. "Arabidopsis thaliana chromosome 1 BAC F27K7 genomic sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
I. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R. REMBL; AC084414; AAG29744.1;
R. RICETPO; IPR000504; RRM.
R. RAMRT; SM00360; RRM; 2.
R. PROSITE; PS50102; RRM; 2.
R. PROSITE; PS50102; RRM; 2.
R. ROSITE; PS50102; RRM, RNP-1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| | :| | | | | 239 KSKDINGDMYMQCDHFFVSCFLKTHWTRKENSPYFFNNENYFIRTLLNKDHLILQSQKNK 298
                                                                                                                                                                                                                                                                                      Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Oquail M.A., Ralyandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668(2000)
Ratuse 403:665-668(2000)
BHBJ. ALISONG, CAMPARJARIAL,
BHBJ. ALISONG, CAMPARJARIAL
SEQUENCE 408 AA: 47256 MW; DD0D034E75EF7C22 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>،</u>
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 101; DB 16; Length 408; 16.0%; Pred. No. 1.2e+03; ive 49; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 49.3%; Score 101; DB 10; Length 557; Best Local Similarity 17.3%; Pred. No. 2.4e+03; Matches 13; Conservative 50; Mismatches 12; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUMI PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 AA.
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                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 16.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 NIIYVSYHSKEDPLT 313
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496 GFVHNFQESN 505

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Ganglia
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 RESULT 13
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                                                                                                                                                                                                                                          Kawasaki H., Springett G.M., Toki S., Canales J.J., Blumenstiel J.P., Chen E.J., Baby I.A., Mochizuki N., Ashbacher A., Matsuda M., Housman D.E., Graybiel A.M., All Novel Rap Guanine Nucleotide Exchange Factor Enriched in the Basal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CALCIUM-AND DIACYLGLYCEROL-REGULATED GUANINE NUCLEOTIDE EXCHANGE
FACTOR I.
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                                                                                                                                                                                                                                                             Query Match
49.3%; Score 101; DB 11; Length 608;
Best Local Similarity 12.9%; Pred. No. 2.9e+03;
Matches 9; Conservative 55; Mismatches 6; Indels (
                                                                                                                                                                                                             Kawasaki H., Housman D.E., Graybiel A.M.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                 608 AA; 69294 MW; DC717794CE12C2D1 CRC64;
                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:13278-13283(1998)
                                      608 AA.
                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
                                      PRT;
                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-99007305; PubMed=9789079;
 242 SKKSSSDESSESED 256
                                      PRELIMINARY;
                                                                                        RASGRP2 OR CALDAG-GEFI.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                      690060
                       RESULT 12
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SEQUENCE FROM N.A.
MEDLINES-99007305; PubMed=9789079;
Kawasaki H., Springett G.M., Toki S., Canales J.J., Harlan P.,
Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A.,
Matsuda M., Housman D.E., Graybiel A.M.;
"A Rap guanine nucleotide exchange factor enriched highly in the basal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawasaki H., Springett G.M., Toki S., Canales J.J., Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A., Matsuda M., Housman D.E., Graybiel A.M.;
"A Novel Rap Guanine Nucleotide Exchange Factor Enriched in the Basal
                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-28001089; PubMed-9341881;
Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
"The germinal center Kinase gene and a novel CDC25-like gene are
located in the vicinity of the PYGM gene on 11q13.";
Hum. Genet. 100:611-619(1997).
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SILING G.U., Grimmond S., Hayward N.;
Silling G.U., Grimmond S., Hayward N.;
"Characterisation of a Novel Nucleotide Exchange Factor.";

REMBL; A12336; CAA730651; -.
REMBL; AF081194; AAC79698.1; -.
REMBL; AF080051; PF0.
Rembl; AF080051; RasGEF. 1.
Rembl; AF080130; DAG_PE-bind; 1.
Rempl; AR00109; C1; 1.
SWART; SW00109; C1; 1.
SWART; SW00109; C1; 1.
SWART; SW00109; C1; 1.
REMBL; AF0811E; PS000479; DAG_PE_BIND_DOM_1; 1.
REMBL; AF0811E; PS000419; DAG_PE_BIND_DOM_2; 1.
REMOSTIE; PS00081; DE_HAND; UNKNOWN_2.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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                                                                  (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 95:13278-13283(1998)
609 AA.
PRT;
                                                                  01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19, F2583.3 KINASE LIKE PROTEIN.
PRELIMINARY;
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XX MEDLINE-20493616; PubMed=10918068;

RA Glyde-Smith J., Silins G., Gartside M., Grimmond S., Etheridge M.,

RA Glyde-Smith J., Silins G., Gartside M., Grimmond S., Etheridge M.,

RA Apolloni A., Hayward N., Hancock J.F.;

RT "Characterization of RasGRP, a Plasma Membrane-targeted, Dual

RT "Characterization of RasGRP, a Plasma Membrane-targeted, Dual

RT "Characterization of RasGRP Exchange Factor.";

LJ Biol. Chem. 275:32260-32267(2000).

CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.

DR HSSP; P28867; 1PTQ.

DR HSSP; P2800613; PAG_FE-bind; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00109; DAG_FE_BIND_DOM_1; 1.

DR SMART; SM00109; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS001018; EF_HAND; UNKNOWN_2.
                                                                                                              Gaps
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                               ;; Score 101; DB 4; Length 609;
;; Pred. No. 2.9e+03;
55; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
Calcium-binding; Phorbol-ester binding.
SEQUENCE 609 AA; 69248 MW; 8B1321F864D24BC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671 AA; 75547 MW; 67B7BD2B4F4AED4D CRC64;
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GUANINE EXCHANGE FACTOR MGG7 ISOFORM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 4;
Pred. No. 3.5e+03;
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y 12.9%; Pred. No. 3...

''' 55; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                49.38;
12.98;
                                   Query Match
Best Local Similarity 12.9*
Onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 12.5.
Local 9, Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                             496 GEVHNFQESN 505
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                                                                                                                                               64 XXXXXXQQSN 73
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SEQUENCE 671
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ID Q9H1B6
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MEDLINE-20553456; Pubmed-11099377;
Goetting C., Kuhn J., Zahn R., Brinkmann T., Kleesiek K.;
Molecular cloning and expression of human UDP-D-xylose:proteoglycan core protein beta-D-xylosyltransferase and its first isoform XT-II.";
J. Mol. Biol. 304:517-528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "First isolation of human UDP-D-xylose:proteoglycan core protein beta-D-xylosyltransferase secreted from cultured JAR choriocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Kuhn J., Goetting C., Schnoelzer M., Kempf T., Brinkmann T.,
Kleesiek K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94490 MW; B4A96EE24F094CCF CRC64;
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
XYLOSYLTRANSFERASE I (EC 2.4.2.26) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 49.3%; Score 101; DB 4; Lv Best Local Similarity 17.3%; Pred. No. 5.5e+03; Matches 13; Conservative 53; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 14, 2002, 15:22:14 Job time: 682 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ27741; CAC16767.1; -.
Transferase, Glycosyltransferase.
NON_TREE SEQUENCE 827 AA; 94490 MW; B41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. 0:0-0(0)
                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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4.5
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model	August 14, 2002, 15:15:34; Search time 230.21 Seconds (without alignments) 114.832 Million cell updates/sec	: US-09-499-662-127 :t score: 1237 !OE: 1 METDILLMVLLLWVPGSTGEVTHQGLSSPVTKSFNRGEC 238	ig table: BLOSUM62DX Gapop 10.0 , Gapext 0.5	ned: 747574 segs, 111073796 residues	Total number of hits satisfying chosen parameters: 747574
OM protein -	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_032802:* Database

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
14: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1992.DAT:*
15: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1993.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti-Fas humanised Humanised anti-Fas Humanised anti-Fas Anti-Fas humanised Anti-Fas humanised Humanised anti-Fas Humanised HFE7A de Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Description SUMMARIES AAW90931 AAW83034 AAB14777 AAW83031 AAB14772 AAW90922 AAW83032 AAB14773 AAW90930 AAW90927 Length DB 2338 2238 2238 2238 2338 2338 Query Match I 1236 1233 1173 1173 1173 1168 1168 11158 Score 20 20 10 11 11 Result Š.

3	19 AAW83035 Anti-Fas h	21 AAB14778 Humanised anti-F	21 AAW90928 Humanise	19 AAW83033 Anti-Fas h	21 AAB14774 Humanised	21 AAW90924 Humanised	18 AAW13563	20 AAW95658	21 AAY85200 Light chain an	22 AAB76947	14 AAR33312 Humanised MaE1	20 AAY50030 Human E27 and	20 AAW95660 Mus	20 AAW95662	21 AAB07472 Amino acid se	22 AAB74211 E27 anti-I	20 AAW95669 Mus musculus	20	22 AAB47087 Anti-IgE ant	22 AAB76949	22 AAB76951 Full leng	22 AAB76953 Variable	22 AAB76958 Variab	21 AAY96298 Human IGI		22 AAB82912	14 AAR38162 Sequence of the	20 AAY50161 Human	21 AAY96301 Human	18 AAW11638 Human	0 22 AAG63665 Amino aci	
93.4	93.3	93.3	93.3	93.2	93.2	93.2	6.68	88.9	88.9	88.9	88.4	87.1	87.1	87.1	87.1	87.1	86.8	86.8	86.8	86.8	86.8	86.8	86.8	85.2	84.8	84.7	84.5	84.4	84.2	84.1	83.0	
1155	1154	1154	1154	1153	1153	1153	1112	1100	1100	1100	1093	1077	1077	1077	1077	1077	1074	1074	1074	1074	1074	1074	1074	1053.5	1049.5	1047.5	0	1044	1041.5	1040	1027	
																								_	-							

ALIGNMENTS

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed light chain Leu 1 protein. AAW90930 standard; Protein; 238 AA 08-AUG-2000 (first entry) AAW90930; RESULT AAW90930

Synthetic.

EP990663-A2

99EP-0307711 29-SEP-1999; 05-APR-2000.

98JP-0276881 98JP-0276882 30-SEP-1998; 30-SEP-1998;

Humanised anti-Fas

(SANY) SANKYO CO LTD.

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This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between the anti-inflammatory, antidiabetic, anti-arthritic, antiviral, immunomodulatory, darmatological, immunosupressive, thyromimetic, antiviral, immunomodulatory, darmatological, antinifertility, neuroprotective, antirheumatic, nephrotropic, antinifertility, neuroprotective, cantinity antidice apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive apoptosis by binding to cell surface Fas or inhibit it by competitive canemia, starility, myasthemic systemic users associated with the Fas/Fas ligand system, especially systemic users. Addison's disease, rheumatoid arthritis, graft versus host disease, soleroderma, Goodpasture syndrome, Codisease, autoimmune hemolytic anemia, starility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (8, C or D) or alcoholic), and transplant rejection. (1) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic multiple a human anti-murine antibody light chain construct designated Leu inducing a human anti-murine antibody light chain construct designated Leu inducing a humanised anti-pas antibody the response. This sequence represents a humanised anti-pad of the invention.
                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                 Takahashi T;
                           Tamaki I,
                           Nakahara K,
                                                                                                                                                                                                                                                                                              263pp; English.
                                 Haruyama H,
                                                                                                                                                                                                                                                                                           Claim 3; Page 156-157;
                                                                                  WPI; 2000-258930/23.
                                                                                                                N-PSDB; AAA11631
                                 Serizawa N,
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ö QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120 121 TFGOGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 100.0%; Score 1237; DB 21; Length 238; 100.0%; Pred. No. 6.7e-62; 1ve 0; Mismatches 0; Indels 0; Query Match 100. Best Local Similarity 100. Matches 238; Conservative 61 61 a ò g g à δ

238 AA;

Sequence

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Humanised anti-Fas designed light chain Leu 3 protein.
                                                 AAW90932 standard; Protein; 238 AA.
                                                                                        08-AUG-2000 (first entry)
                                                                     AAW90932;
181
                             RESULT
AAW90932
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antiheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Slorgen's syndrome; crohn's disease; scleroderma; sterility; Godgasture syndrome; crohn's disease; sclerility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. antidiabetic; Fas; antibody; human; anti-inflammatory; anti-anemic;

EP990663-A2 Synthetic.

05-APR-2000

99EP-0307711. 29-SEP-1999; 98JP-0276881. 98JP-0276882. 30-SEP-1998; 30-SEP-1998;

(SANY) SANKYO CO LTD.

Haruyama H, Nakahara K, Tamaki I, Takahashi T; Serizawa N,

WPI; 2000-258930/23. N-PSDB: AAA11633 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 161-162; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cells with an abnormal Fas/Fas

capoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-anemic, antidiabetic, anti-allergic, anti-arthritic, anti-irral,

cation-teriosclaerotal, cardiant and hepatropic activity. (I) induce

antirheumatic, nephrotropic, antinfertility, neuroprotective,

cantinheumatic, nephrotropic, antinfertility, neuroprotective,

cantinheumatic, nephrotropic, antinfertility, neuroprotective,

cantinheumatic, nephrotropic, antinfertility, neuroprotective,

cantinheumatic, nephrotropic, antinfertility, neuroprotective,

capoptosis by binding to cell surface Fas or inhibit it by competitive

capoptosis by binding to cell surface Fas or inhibit it by competitive

capoptosis by binding to cell surfacese, remarked arthritis, graft

versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

lupus erythematosus, Hashimoto disease, thrombopenia purpura, insulin

canemia, Addison's disease, scleroderma, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arterioscleroals, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral

Cardiomyopathy, glomerulonephritis, so can be evaluated in

calls. They bind to both human and murine Fas, so can be evaluated in

calls. They bind to both human and murine Fas, so can be evaluated in

calls. They bind to both human and murine Fas, so can be evaluated in

calls. They bind to mor induce liver disease, and have reduced risk of

inducing a human anti-wurin

Sequence

ö Gaps ô Length 238; Indels Score 1236; DB 21; Pred. No. 7.6e-62; 1; Mismatches 0; 99.98; Query Match Best Local Similarity 99.6 Matches 237; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotroptc; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule (1) that, induces approasis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells. With a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, anti-antirematic, nephrotropic, anti-infertility, neuroprotective, anti-arteriosclerctic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanized anti-Fas'antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                   This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi T;
                                                                                                                                                                                                                                                                                                   Humanised anti-Fas designed light chain Leu 2 protein.
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                                                                                                                                                                                                                         AAW90931 standard; Protein; 238 AA
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-258930/23.
N-PSDB; AAA11632.
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diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OOKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCOOSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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Sjogren syndrome; pernicious anaemia; Addison's disease;
scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.7%; Score 1233; DB 21; Length 238; 99.6%; Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFE7A; monoclonal antibody; mouse; Fas; humanised antibody:
apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Fas humanised antibody HFE7A light chain PDHH type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.1e
1; Mismatches
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21..238
/label= Mat_protein
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/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.6 Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW83034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

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chain of murine anti-human feas monoclonal antibody HFB7A.

Humanisation of the murine sequence (see AAW83042) entailed making

Enter Agray, K498, H805, P81R, V82L, E84P, A87F, T89V and R107K

munic acid substitutions; these residues are conserved in the

human light chain (kappa chain). Host cell Escherichia coli

phSHH5 SANK 7039B harbors plasmid phSHH5 carrying a fusion

fragment of the humanised PDHH type HFB7A light chain and DNA

encoding the region of human immunoglobulin kappa chain, and is

deposited as FERW BP-6274 (claimed). The invention provides

methods for producing humanised antibodies by culturing host

cells. Humanised versions of HFB7A (see AAW83011-37), like native

HFB7A, are capable of inducing apoptosis in abnormal cells

cells. The humanised antibodies are used to evaluate, in animal

cells. The humanised antibodies are used to evaluate, in animal

cells. The humanised antibodies are used to sealuate, in animal

cells. The humanised settlematosus, Hashimoto's disease,

cells. Tystemic lupus erythematosus, hashimoto's disease,

crimeractions, and also to treat such diseases, including autoimmune

disease (e.g. systemic lupus erythematosus, hearing and an animal

disease, theumatodia arrayis untoimmune haemolytic anaemia,

sterility. Mysathbolis arrayis multinibe solarose, heamenia,

sterility. mysathbolis arrayis multinibe solarose.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the PDHH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                          in O, Kimihisa I;
Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Jun 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Page 218; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hiroko Y, J
S, Shin Y,
                                                                                    74..80
/label- CDR_L2
/note- "claim 9"
                                                                                                                                        113..121
/label= CDR_L3
/note= "claim 9"
                 'label - Constant
                                                                       /note= "claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myocarditis, hepatitis and AIDS
                                  44..58
/label- CDR_L1
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97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hideyuki H,
O, Nobufusa
                                                                                                                                                                                                                                                                                                                                                                                                       (SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                        30-MAR-1998;
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25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masahiko O,
                                                                                                                                                                                                                   AU9859701-A
                                                                                                                                                                                                                                                     08-OCT-1998
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                                                                                          Region
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Region
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFF7A containing identical CDRs (complementarity determining regions) to antibody HFF7A, Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, actopy arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AABI4777-B14778 represent the light chains of several humanised HFF7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent for the diseases caused by an abnormality
181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                        the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised anti-Fas antibody light chain, SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 101; 139pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                       AAB14777;
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238 AA;

Sequence

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Gaps

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94.8%; Score 1173; DB 19; Length 238; 92.9%; Pred. No. 2.4e-58; ive 10; Mismatches 7; Indels 0

Local Similarity 92.9 ses 221; Conservative

Matches

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-allergi; anti-arthritic, antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinnertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-allocyic, anti-allocyic, anti-incompanient of anti-allocyic, anti-arthritic, antivial, immunosuppressive, thyronimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                              TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                            QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                               METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                       antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                   Indels
Pred. No. 2.4e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised HFE7A designed light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 141-142; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                     AAW90927 standard; Protein; 238 AA.
   92.98; Pic. 7
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98JP-0276882.
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                  11 Similarity 92.9
221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SANY ) SANKYO CO LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP990663-A2
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                Best Local
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
anemia, Addison's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic Lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 1173; DB 21; Length 238; 92.9%; Pred. No. 2.4e-58; 1ve 10; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-Fas humanised antibody HFE7A light chain HH type.
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.8'
Best Local Similarity 92.9'
Matches 221; Conservative
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Synthetic.
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Peptide
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QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120

181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

AAB14772 standard; Protein; 238

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AAB14772 RESULT

(first entry)

24-NOV-2000

AAB14772;

121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

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Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
21..238
/label= Mat_protein
                                                         /note= "claim 9"
113..121
/label= CDR_L3
          21..131
/label= Variable
                          /label- Constant
                                         /note= "claim 9"
                                                                         note= "claim 9"
                                                                                                                                                                                                 myocarditis, hepatitis and AIDS
                                               74..80
/label= CDR_L2
                                44..58
/label= CDR_L1
                                                                                                                        97JP-0082953
97JP-0169088
                                                                                                         98AU-0059701
                                                                                                                   97JP-0276064
                     .32..238
                                                                                                                                        (SANY ) SANKYO CO LTD.
                                                                                                                                                                 WPI; 1998-543440/47.
                                                                                                                                                                       N-PSDB; AAV70074
                                                                                                         30-MAR-1998;
                                                                                                                   08-OCT-1997;
                                                                                                                        01-APR-1997;
25-JUN-1997;
                                                                                    AU9859701-A
                                                                                               08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                            Sequence
 Protein
           Region
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murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardicomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.

Chimeric - Mus musculus. Chimeric - Homo sapiens.

JP2000169393-A.

99JP-0278301.

30-SEP-1999;

20-JUN-2000

Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; Humanised anti-Fas antibody light chain, SEQ ID NO:50.

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chain of murine anti-human Fargeners of the murine anti-human Esquence (see AAM83042) entailed making P47A, K49R, H80S, P81R, V82L, E89H, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised H type HFE7A light chain and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A carrying host cells. Humanised versions of HFE7A carrying host cells. The humanised cantibodies by culturing host cells. The humanised versions of HFE7A care apoptosis in abnormal cells expressing Fas, and of inhibiting apoptosis in normal cells. The humanised antibodies care used to evaluate, in animal models, treatments of diseases that involve FasyFas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma. Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetees), allergies, attopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the HH type humanised light
                                                                                                                                                                                                                                                                                             Claim 21; Page 199-199; 292pp; English.
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy. Gallergy, atopy, atteriosclerosis, myocarditis, cardiomyopathy. AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 78-79; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0276883.
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238

Sequence

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Gaps

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Length 238; Indels

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94.4%; Score 1168; DB 19; 92.4%; Pred. No. 4.6e-58; ive 10; Mismatches 8;

Conservative

Similarity

Local Simi hes 220;

Best Loca Matches

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyronimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                           QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                         121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                  Gaps
                                                                               1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                      GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                       This invention describes a novel humanized anti-Fas antibody-like
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 Length 238;
                                 Indels
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 DB 21;
94.4%; Score 1168; DB 21
92.4%; Pred. No. 4.6e-58;
ive 10; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                 AAW90922 standard; Protein; 238 AA.
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                               220; Conservative
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              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999;
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cast and its ligator. The products of the invention and its ligator. The products of anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, inmunomodulatory, dermatological, immunosuppressive, thyromimetic, antiatheumatic, nephrotropic, antiinfertility, neuroprotective, antiateriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive, inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Solegen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myccarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. C or D) or alcoholic), and transplant rejection. (1) selectively induce it in abnormal
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                                                                                                                                                                                                                                                                                                                                                                                            mimic
                                                                                                                                                                                                                                                                                                                                                                cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFRTA light chain HH type which is used in the method described in the invention.
and its ligand. The products of the invention have anti-inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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92.4%; Pred. No. 4.6e-58;
ive 10; Mismatches 8
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Synthetic.
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Matches 220;
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Location/Qualifiers
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                                                                                      WPI; 1998-543440/47.
N-PSDB; AAV70075.
                                                          30-MAR-1998;
                                                                 01-APR-1997;
                                                                    25-JUN-1997;
                                                               08-OCT-1997;
                                                                                 Masahiko O,
                                                AU9859701-A
                                                     08-OCT-1998
                                                                              Akio S,
  Peptide
       Protein
             Region
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                       Region
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Sequence

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This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making p47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coll p46GHM17 SANK 7397 harbors plasmid pHSGHM17 carrying a fusion fragment of the humanised and immunoglobulin kappa chain, and is encoding the region of human immunoglobulin kappa chain, and is emposited as FERW BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW8301-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus expthematosus, Hashimoto's disease, condessing actiones, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus expthematosus, Hashimoto's disease, creinist seemic lugus expthematosus, Hashimoto's disease, scleroderma, Goodpasture syndrome, Crobn's disease, rheumatoid arthritis, autoimmune emplytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, hypoplastic anaemia, hepatitis, hypoplastic anaemia, hepatitis, hypoplastic anaemia, hepatitis, acidiomyopathy, glomerular rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
O, Nobufusa S, Shin Y, Tohru T;
/label= Sig_peptide
21..238
/label= Mat_protein
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                                                                                                                           21..131
/label= Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113..121
/label= CDR_L3
/note= "claim 9"
                                                                                                                                                                                                                                                  /label= Constant
                                                                                                                                                                                                                                                                                                                                                                             'note= "claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "claim 9"
                                                                                                                                                                                                                                                                                            44..58
/label= CDR_L1
                                                                                                                                                                                                                                                                                                                                                                                                                   74..80
/label= CDR_L2
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97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; attopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                                                                                                      QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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   Length 238;
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                                                                           Indels
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93.4%; Score 1155; DB 19; 91.6%; Pred. No. 2.4e-57;
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                                                                           11; Mismatches
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                                                                       Matches 218; Conservative
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Chimeric - Homo sapiens.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; antialergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashlmoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                              QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                             121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                         Gaps
                                                                                           1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                        GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory or autoimmune disease, induces apoptosis selectively cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                               Humanised anti-Fas antibody HFE7A light chain HM type protein.
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                                                                       Indels
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                                                    ; be 2.4e-57; 9;
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                                                                       11; Mismatches
                                                  93.4%; Score 1155;
                                                               Pred. No.
                                                                                                                                                                                                                                                                                               AAW90923 standard; Protein; 238 AA.
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                                                               91.68;
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                                                                       Conservative
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                                                              Similarity
                     238 AA;
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                                                              Best Local Sim.
Matches 218;
antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                      AAW90923;
                     Sequence
                                                  Query Match
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Injured system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antishemmatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell sufface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic nemain, Addison's disease, cleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myssthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral) (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFETA light chain HM type which is used in the method described in the invention.
induces apoptosis in cells with an abnormal Fas/Fas
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Pred. No. 2.4e-57;
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Best Local Simi
Matches 218;
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238 AA;

Sequence

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chain of murine anti-human Psagance of the multipody HFEFA.

Kumanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coli pHSHMZ SANK 70198 harbors plasmid pHSHMZ carrying a fusion of the humanised PDHM type HFEFA light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERN BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells. Kyressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune classase, graft versus host disease, Sjogren syndrome, pernicious anaemia, disease, rheumatoid arthritis, autoimmune haemolytic anaemia, starility musarthenia matining multimine haemolytic anaemia, starility musarthenia multimine haemolytic anaemia. New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS This is the amino acid sequence of the PDHM type humanised light Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I; Masahiko O, Nobufusa S, Shin Y, Tohru T; Claim 21; Page 220-221; 292pp; English. /label- Sig_peptide label = Mat_protein ocation/Qualifiers 74..80 /label- CDR_L2 /note= "claim 9" /113..121 /label= CDR_L3 /note= "claim 9" 21..131 /label= Variable 'label - Constant 'note- "claim 9" 14..58 /label= CDR_L1 97JP-0276064. 98AU-0059701 97JP-0082953 97JP-0169088 132..238 (SANY) SANKYO CO LID. WPI; 1998-543440/47. N-PSDB; AAV70078. 08-OCT-1997; 30-MAR-1998; 01-APR-1997; 25-JUN-1997; AU9859701-A 08-OCT-1998

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autolimune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                              61 QQKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                           121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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        Length 238;
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                                           Indels
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Score 1154; DB 19;
Pred. No. 2.7e-57;
                                           11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             AAB14778 standard; Protein; 238 AA.
          93.3%;
91.6%;
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                         Best Local Similarity 91.6
Matches 218; Conservative
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-Fas antibody
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            Query Match
Best Local $
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Example reference 21; Page 144-145; 263pp; English.

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glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
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                                                                                                                                                Indels
                                                                                                                   93.3%; Score 1154; DB 21;
91.6%; Pred. No. 2.7e-57;
ive 11; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised HFE7A designed light chain protein #2.
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                                                                                                                                   Best Local Similarity 91.6
Matches 218; Conservative
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                                                                       238 AA;
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molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antificumatic, nephrotropic, antificentility, neuroprotective, antistreriosclerotic, acidiant and hepatropic activity. (1) induce antistreriosclerotic, cardiant and hepatropic activity. (1) induce antistreriosclerotic, cardiant and hepatropic activity. (1) induce inhibition of ligand binding. (2) are used to treat and/or prevent inhibition of ligand binding. (3) are used to treat and/or prevent classes associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
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                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like
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91.6%; Pred. No. 2.7e-57
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11; Mismatches
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Job time: 832 sec
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Query Match
Best Local Similarity
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RESULT
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(without alignments)
70.141 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19,
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1237
1 METDIILLWVLLLWVPGSTG......EVTHQGLSSPVIKSFNRGEC
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
                            4.5
Compugen Ltd.
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US-08-466-163B-9
US-09-282-505-1
US-09-054-255-1
US-08-887-352B-15
US-08-887-352B-17
US-08-887-352B-17
US-09-109-207C-17
US-09-109-207C-17
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US-09-109-207C-13
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PCT-US93-07832-39
US-07-934-373C-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-07832-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 protein search, using sw model
                                                                                                                                                                                      August 14, 2002, 15:17:03
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Gapop 10.0 , Gapext 0.5
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Maximum |
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                                                                                                                                                                                                                                                                                           Title:
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APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ ?
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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6, O Appli
10, Appli
10, Appli
2, Appli
2, Appli
62, Appli
62, Appli
67, Appli
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Pred. No. 1.6e-87;
US-08-788-800-11

US-08-437-642B-40

US-09-097-309-2

US-09-097-309-2

PCT-US9-0783Z-40

US-09-097-309-6

US-09-097-309-6

US-09-171A-10

US-09-027-712B-2

US-09-027-49-62

US-09-027-449-51

US-09-027-449-51

US-09-027-444-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-72

US-09-026-985-72
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASC11
CURRENT APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP 95 114 969.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9613152 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 E
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Ha
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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98.2%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
            STRANDEDNESS: single
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CLASSIFICATION:
        TOPOLOGY:
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121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                  141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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   Gaps
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                                     21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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   2; Indels
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03.011-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGMA CATAIQ G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91.123
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 1.7e-86;
2; Mismatches 3;
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                                                                                                                                                                                                                                                                 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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97.7%;
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Matches 214; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-08-887-352B-13
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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Pred. No. 1.7e-86;
2; Mismatches 3; Indels
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTONNEY/AGGNT INFORMATION:
NAME: SVODOGA, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
                                                                                                                                    Sequence 9, Application US/08466151
Patent No. 6037453
                                                                                                                                                                                                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity 97.7%;
Matches 213; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                    US-08-466-151-9
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                                                                                                                                                                     21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                                                                                               Length 218;
   ; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
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                                                                                                                                Indels
                                                                                             Score 1100; DB 4;
Pred. No. 1.7e-86;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 88.9%; Score 1100; DB 4;
Best Local Similarity 97.7%; Pred. No. 1.7e-86;
Matches 213; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT FILING DATE: 1995-06-06
CURRENT FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                   181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
                                                                                             Query Match 88.9%;
Best Local Similarity 97.7%;
Matches 213; Conservative
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CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER RAPLICATION DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
                                                                                                                                                                                                                                                         APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1 CURRENT FILID POLYPEPTION NUMBER: US/09/109,207C CURRENT FILID DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44 SEQ ID NOS: 44
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141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%; Score 1100; DB 4; Length 218; 97.7%; Pred. No. 1.7e-86; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Artificial
LOCATION: 1-218
CHER INFORMATION: Light chain sequence derived from MAE11
MS-09-109-207C-13
                                                                      STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-109-207C-13
Sequence 13, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
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Best Local Similarity 97.7'
Matches 213; Conservative
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                               61 GVPSRFSGSGGGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
                                           81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                    121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997

CLASSIFICATION: 530
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Pred. No. 2.8e-84;
5; Mismatches 5;
                                                                                                                                                                                                            STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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NAME: SVODOda, Craig G.
REGISTATION UNDRER: 39,044
REFERENCE/DOCKET UNDRER: P112:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
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STATE: California
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Best Local Similarity 95.4%;
Matches 208; Conservative
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Amino Acid
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Pred. No. 1.6e-84;
4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Sequence is completely synthesized ; Patent No. 6194551 US-09-282-505-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: E27 anti-1gE antibody light chain US-09-054-255-1
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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Patent No. 6242195;
GENERAL INFORMATION:
APPLICANT: Esobe Ekinaduese Idusogie et al.;
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255;
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
                                                                                                    Sequence 1, Application US/09282505A Patent No. 6194551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%;
95.9%;
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Artificial Sequence
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Best Local Similarity 95.9°
Matches 209; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 218
                                                                              US-09-282-505-1
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLFISSLQPEDFATYYCQOSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 2.8e-84;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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                                                                                                                                                 COMPUTER: 13.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                   STREET: 1 DNA Way
STREET: 2 South San Francisco
STATE: California
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Best Local Similarity 95.4%;
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 amino acids
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650/952-9881
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  CORRESPONDENCE ADDRESS
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SOFTWARE: WinPati
                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                        STATE: Cali:
COUNTRY: USI
ZIP: 94080
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 218;
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Pred. No. 2.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/887,352B TILING DATE: 03.3-101-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08887352B Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonar TITLE OF INVENTION: Improved Anti-TITLE OF INVENTION: Improving Poly
                                                                                                             Sequence 17, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9001
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.8
Best Local Similarity 95.4
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-887-352B-17
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US-08-887-352B-19
                                                                  RESULT 10
US-08-887-352B-17
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Gaps ; 0

us-09-499-662-127.rai

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Sequence 17, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
FILE REFERENCE: P1123R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
TITLE OF INVENTION: Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
FILE REFERENCE: P1123R1
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               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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86.8%; Score 1074; DB 4;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5;
                                                                                                                                                                                          STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/109, 207C CURRENT FILING DATE: 1998-06-30
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SEQ ID NO 19
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Artificial
                                                                                                                                                                                                                                                                       RESULT 14
US-09-109-207C-17
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LENGTH: 218
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%; Score 1074; DB 2; 95.4%; Pred. No. 2.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1074; DB 4;
Pred. No. 2.8e-84;
5; Mismatches 5;
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....ек: US/08/887,352B
03-Jul-1997
N: 530
тиг. 530
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                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                         REFERENCE/DOCKET NUMBER: PI.
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650/255-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
95.4%;
                                                                                                                                                                                                                                                                                         LENGTH: 218 amino acids TYPE: Amino Acid
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 208; Conservative
                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 US-08-887-352B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                   ) ORGANISM: Artificial

; FEATURE:

; NAME/RE: Artificial

; LOCATION: 1-218

; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11

US-09-109-207C-19
                                                                                                                 ó
                                                                                         Length 218;
                                                                                       Query Match

86.8%; Score 1074; DB 4; Length 2
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

SUMMARIES

Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain v r Ig kappa chain - m Ig kappa chain yr Ig kappa chain pre Ig kappa chain (WM Description S42772 S16112 JL0029 A20969 S52059 PT0219 S29593 JC5810 S01320 A31790 A56169 S37484 PC4203 18865 15058 12028 JE0242 JE0244 JE0243 A23746 JE0241 S06084 833161 % Query Match Length DB 716.5 7709.5 7706.5 7706.5 7706.5 697 697.5 677.5 608. 945.5 926.5 903.5 885.5 877 809 756 749 748.5 Score Result No.

F.; Yamaki, S.; Kazi, H.

A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL A; Reference number: JE0243

A;Accession: JE0244 A;Molecule type: protein A;Residues: 1-215 <ALL> C;Superfamily: immunoglobulin V region; immunoglobulin homology

A49633 K3HU

Ig kappa chain NIG2 precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C;Accession: JE0244 R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; submitted to JIPID, November 1998

STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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Ig kappa chain pre Ig kappa chain pre Ig kappa chain - h Ig kappa chain v-J Ig light chain - r Ig kappa chain v-I Ig kappa chain v-I Ig kappa chain v-I Ig kappa chain c	an on 05-Dec-1998 #text_change 21-Jan-2000 .S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda p of kappatype light chains with AL amyloidosis: on; immunoglobulin homology	tch 76.4%; Score 945.5; DB 2; Length 215; al Similarity 83.5%; Pred. No. 1.2e-54; 182; Conservative 15; Mismatches 18; Indels 3; Gaps 1; DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80 :
PL0106 KVMSM6 S40331 S29577 KVMS32 KVMS32 RVMS32 S20653 S20653 S20653 S20653 S20653 S20653 S20653 S20653 S20653 S20653	ALIG - human revision 0: ain, M.S.; 998 tonship of v region;	18; Score 58; Pred. 15; Mis TITCKASOSVI 1::1:1111 FLSCRASOSV- SSLOPEDFATY 1:11111
ппопринопини	or - } 2_rev' \$sain, \$sain, \$1998 \$tions	48; 58; TILS TILS SSI
144 1233 127 1233 1327 131 145 145 131 131 131 131	AL. precursor - human mans (man) #sequence_revision "S.; Hossain, M.S November 1998 tture relationship of JE0241 otein Li> noglobulin V region noglobulin homolog	larity 83.5%; Conservative 35.5%; PSSLSASVGDRVTITC : : :: PGTLSLSPGERATLSC GSGSGTDFTLTISSL
44444444444444444444444444444444444444	NIG26 pre sales properties proper	tch al Similarity 83.59; Pred. 182; Conservative 15; Mi DIVLTQSPSSLSASVGDRVTITCKASQSV :
547 532 532 520 520 511 511 504 504 699 699	RESULT 1 JE0242 JG kappa chain NIG26 precursor - human C: Specias: Homo sapiens (man) C: Accession: JE0242 SFALIM, M.A.; YamaKl, S.; Hossain, M.S. submitted to JIPID, November 1998 A; Bescription: Structure relationship o A; Reference number: JE0241 A; Nolecule type: protein A; Residues: 1-215 < ALI> C; Superfamily: immunoglobulin V region; F; 16-91/Domain: immunoglobulin homology	a O
	RESULT JE0242 19 kappa C; Speciec C; Date: C; Access R; Alim, submitte A; Descrie A; Refere A; Access A; Molecu C; Superf F; 16-91/	Query M Best Lo Matches Qy 21 Db 1 Qy 81 Db 58

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C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                  Query Match 71.6%; Score 885.5; DB 2 Best Local Similarity 81.6%; Pred. No. 9.5e-51; Matches 177; Conservative 14; Mismatches 23.
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                         A.Molecule type: protein
A.Residues: 1-215 <LEO>
C.Superfamily: immunoglobulin V region; immuno
C.Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
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  preliminary
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C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JE0243
S.A.Him, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998
A.Rescription: A new subgroup of k type light chains (VkV) identified in cases of A.Reference number: JE0243
A.Reference number: JE0243
A.Reference protein
A.Residues: 1-215 <ALI>C.Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 81.7%; Pred. No. 6.5e-52;
Matches 179; Conservative 16; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                              Query Match 74.9%; Score 926.5; Best Local Similarity 83.1%; Pred. No. 2.1e Matches 182; Conservative 14; Mismatches
  immunoglobulin homology <IMM>
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F;16-90/Domain:
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Mucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin k.A;Reference number: S06084; MUID:90016888
A;Accession: S06084
A;Accession: S
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Pred. No. 9.8e-46;
.; Mismatches 52; Indels
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64.6%; Pre-
tive 31;
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Best Local Similarity 60.55
Matches 144; Conservative
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Matches 155
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C; Species: Mus musculus (house mouse)
C; Date: 24-Aug.1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Date: 24-Aug.1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: $68241; $68241
R; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka. submitted to the EMBL Data Library, March 1994
A; Description: Specific peroxidase activity by formation of an antibody L-chain-porph A; Reference number: $68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:D29670; NID:9473962; PIDN:BAA06141.1; PID:9473963
R; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, FEBS Lett. 375, 273-276, 1995
A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A; Reference number: S68211; MUID:96085223
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A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: S33161
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-230 <FOL>
A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin homology <IMM>F:143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPARFSGSGGGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ELVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLATNLES
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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6.9e-42;
ches 47;
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N;Alternate names: immunoglobulin light chain
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A; Residues: 'NI', 3-212 <TAW>
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R;Foley, R.C.; Beh, K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-218 <TAK>
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A; Status: preliminary
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DB 2;

Score 748.5;

60.5%;

Query Match

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A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-234/Product: Ig kappa chain #status predicted <MAT>F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                             Query Match
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A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A; Reference number: JC5810; MUID: 98063277
A; Reference number: JC5810
A; Molecule type: protein
A; Residues: 1-218 < AKA>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C;Accession: S01320
R;de Waele, P: Feys, V; von de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: S01320; MuID:88329081
A;Accession: S01320
A;Molecule type: mRNA
A;Residues: 1-234 <DEL>
A;Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
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                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                               66 KAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQG 125
                                                                                                                                                                                                  126 TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
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                                                                        21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                      Indels
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Pred. No. 9.3e-42;
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                    Mismatches
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   Pred.
                    36;
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64.7%;
 62.2%;
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Matches 141; Conservative
                    145; Conservative
Best Local Similarity
Matches 145; Conserv
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Ci Species: Mus musculus (house mouse)
Cj Species: Mus musculus (house mouse)
Cj Species: Mus musculus (house mouse)
Cj Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
Cj Accession: A31790
Rj Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for A; Reference number: A92686; WUID:89034213
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                                                                                                                                                                                                                                                                                                                                                        RQNGYLNSWIDQDSKDSTYSMSSTLILIKIKDEYERHNSYICEATHKISTSPIVKSFNRNEC 234
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                                                                                                            QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                           8;
  Length 234;
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C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49;
58.9%; Score 729; DB 2; 58.3%; Pred. No. 1.5e-40; ive 37; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.7%; Score 726; DB 2; 61.8%; Pred. No. 2.2e-40;
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                                             Conservative
                       Best Local Similarity
Matches 140; Conserv
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A; Molecule type: mRNA
A; Residues: 1-220 <SCH>
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Search completed: August 14, 2002, 15:18:58
Job time: 686 sec
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Best Local Simi
Matches 131;
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000 C;Accession: A56169  
R;Monfardini, C.; Rieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum A. Biol. Chem. 270, 6628-6638, 1995  
A;Title: Recombinant antibodies in bioactive peptide design. A;Reference number: A56169; MUID:95204454  
A;Accession: A56169  
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-210  
A;Accession: C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accesion: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Reference number: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:q406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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61.8%; Pred. No. 9.2e-40;
iive 29; Mismatches 53;
                                                                                                                                                                                                                                                          58.0%; Score 718; DB 2;
65.1%; Pred. No. 6.8e-40;
iive 28; Mismatches 45;
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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
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                    SEQUENCE (BENCE-JONES PROTEIN AG).
MEDIINE=69234734; PubMed4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Blol. Chem. 244:3550-3560(1969).
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-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A HEAVY CHAIN).
V -> L (IN INV(1,2) MARKER).
/FIId-VAR_003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
51984D1FDD372CE8 CRC64;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
If kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
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                                                                                                       SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU). MEDLINE-70201507; PubMed-5447531;
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57 E
11609 MW;
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InterPro; IPR003597; Ig_cl.
Pfam: PF00047; ig. 1.
SMART: SM00407; IGcl: 1.
PROSITE; PS00290; IG_MHC; 1.
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106
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106 AA;
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KV3I_MOUSE
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McKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSM6.
HSSP; PO1789; IMCP.
InterPro; IPR003596; Ig_MC.
InterPro; IPR003596; Ig_V.
SMART; SMO0406; IG': 1.
Immunoglobulin V region; Signal.
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MEDLINE-78235887; PubMed-98179;
MISTAGE 11,

"Durstein Y., Schechter I.,

"Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       McKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence variation among
kappa chains with limited sequence differences.";
Blochemistry 12:760-771(1973).
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43.0%; Score 532; DB 1;
Best Local Similarity 75.6%; Pred. No. 4.6e-36;
Matches 99; Conservative 18; Mismatches 14,
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21-JUL-1986 (Rel. 01, Last sequence update)
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BY SIMILARITY.
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                                                                                                                                                                                                                                  SEQUENCE OF 21-131.
MEDLINE=73140225; PubMed=4691517;
                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
MEDLINE-79012520; PubMed-99744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14291 MW;
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|121 TFGGGTKLEIK 131
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21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
Loh E., Schilling J., Hood L.E.; information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                             12002 MW; 7A5FCB586C306D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                39.0%; Score 483; DB 1; ilarity 81.1%; Pred. No. 3.1e-32; Conservative 10; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
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BY SIMILARITY
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HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                    PIR; A01937; KVMS43.
HSSP; P01789; 1MCP.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Weigert M., Gatmaitan L., "Rearrangement of genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11952
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Nature 276:785-790(1978).
                                                 Nature 276:785-790(1978).
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Best Local Similarity
Matches 90; Conserv
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KV3N_MOUSE
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-!- MISCELLANEDUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MODE 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
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                                                                                                                                                                            SEQUENCE OF 21-132.
MEDLINE-7314024; PubMed-4120629;
MEDLINE-7314 Poot I.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                               Burstein Y., Schechter I., Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7043.
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                                                                                                                         expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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MEDLINE=79073152; PubMed=103003;
               SEQUENCE OF 1-37.
MEDLINE=78235887; PubMed=98179;
                                                                                                                                                                                                                                                                                                                                                          PIR; A01933; KVMS32.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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132 AA;
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Les 90; Conserv
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P01665;
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KV30_MOUSE
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                                           21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                    81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRFFGQGTKVEIK 131
38.9%; Score 481; DB 1; Length 111; 80.2%; Pred. No. 4.5e-32; ive 11; Mismatches 11; Indels
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                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-I region Walker precursor.
Homo sapiens (Human).
                                                                                                                                                                    129 AA
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                     89; Conservative
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129 AA;
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                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E., "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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80.2%; Pred. No. 6.4e-32;
iive 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region HAH precursor.
                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 6308.
                                                                                                                                                                                         111 AA.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; C01937; KVMS08.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig'. IG_NSMRRT; SM00406; IGv; 1
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 276:785-790(1978).
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Best Local Similarity 80.23
Matches 89; Conservative
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                                                      121 TFGQGTKVEIK 131
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SEQUENCE FROM N.A.
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KV3L_MOUSE
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Best Local S.
Matches 88
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                                                                                                                                                                                                                                                                                                                                      Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. EXP. Med. 167:840-852(1988).
-!- DIERARE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAJUVANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                       DB 1; Length 129;
                                                                                                                                                            IG KAPPA CHAIN V-III REGION HAH.
FRAMEWORK-1.
COMPLEMENTARIIY-DETERMINIG-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                         14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                     38.7%; Score 478.5; DB 1
68.9%; Pred. No. 8.5e-32;
ive 17; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA.
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BY SIMILARITY.
MEDLINE=88171307; PubMed=3127527;
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MEDLINE=79073152; PubMed=103003;
                                                                                                                      Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; E01937; KVMS69.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                 PIR; PL0022; K3HUHA.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Best Local Similarity 68.99
Matches 91, Conservative
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129 AA;
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ID KV3Q_MOUSE
AC P01669;
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DISULFID
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MEDLINE-79.

MEDLINE-79.

MCKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-!- MISCELIANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN.

PIR: A01936; KWMSC1.

InterPro; IPR003006; Ig_MRC.

InterPro; IPR003006; Ig_W.

Pfam: PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Inmunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY - DETERMINING - 3.
FRAMEWORK - 4.
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 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                      38.5%; Score 476; DB 1; Length 111; 79.3%; Pred. No. 1.1e-31;
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COMPLEMENTARITY-DETERMINING-2.
                                                 COMPLEMENTARITY - DETERMINING - 2.
                                                                                   COMPLEMENTARITY - DETERMINING - 3
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                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                      12011 MW; 6FAA345279356829 CRC64;
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78.4%; Pred. No. 4.9e-31;
iive 12; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
Mus musculus (Mouse).
                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA
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                                                                                                                     BY SIMILARITY.
                                   FRAMEWORK-2.
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21-JUL-1986 (Rel. 01, Last seq
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111 AA;
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Best Local Similarity
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   24
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RESULT 11 KV1H_HUMAN

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21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Ripps T.J., Tomhave E., Chen P.P., Carson D.A.;
Rudontibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-1- DISEASE: THE PROPEIN IS ONE AUTH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                  COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
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COMPLEMENTARITY - DETERMINING - 2.
FRAMEWORK - 3.
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                                                                                                                                                                                                                                                                                69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                                                       37.1%; Score 458.5; DB 1;
78.4%; Pred. No. 2.8e-30;
tive 11; Mismatches 12;
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                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-III region HIC precursor.
Homo sapiens (Human).
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FRAMEWORK-1
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HSSP, POLT98; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Fram; PP00047; ig; 1.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Signal.
                                                    PIR; D01937; KVMST0.
HSSP, P01789; INCP.
InterPro; IPR003506; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                11950 MW;
                             diversity.";
Nature 276:785-790(1978).
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Best Local Similarity 78.43
Matches 87; Conservative
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110 AA;
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SEQUENCE FROM N.A.
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  Weigert M.,
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NON_TER
SEQUENCE
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KV3M_HUMAN
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                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=71032830; PubMed=4097974;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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; Pred. No. 1.7e-30;
11; Mismatches 7; Indels
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08D3A6160D8D0618 CRC64;
                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7210.
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DOMAIN 1 23 FRAMEWORK-1.
                                                                                 108 AA
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                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 F.R.
49 F.W.
56 C.O.
97 C.O.
107 F.R.
88 B.Y.
1107 F.R.
1167 MW; (
                                                                                                                                                  Ig kappa chain V-I region Hau.
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80.4%;
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                                                                                 STANDARD;
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P01668;
                                                                                 KV1H_HUMAN
P01600;
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Best Loca Matches

KV3P_MOUSE

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Length 110;

81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132

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                                                                                                                                                                                                                                                                                                                        61 QOKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                            MEDILNE-75059122; Pubmed-4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Laure C.J., Watanabe S., Hilschmann N.;
The primary structure of a monoclonal Igh-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.,
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                            3;
                                                                                                                                                  DB 1; Length 129;
  COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
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Pred. No. 9e-30;
8; Mismatches 11; Indels
                                                                                                                                             Query Match 36.9%; Score 456.5; DB 1; Length Best Local Similarity 67.4%; Pred. No. 4.9e-30; Matches 89; Conservative 17; Mismatches 23; Indels
                                                                                      14070 MW; 7395528EA2BB74D6 CRC64;
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P01599;
21-JUL-1986 (Rel. 01, Created)
15-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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79.5%;
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HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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129 AA;
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MEDLINE-77038198; PubMed=824717;

A Capra J.D., Klapper D.G.;

Tigh anti-gamma globulins (Lay/Pom) with shared idiotypic

To matti-gamma globulins (Lay/Pom) with shared idiotypic

To matti-gamma globulins (Lay/Pom) with Shared idiotypic

Tigh anti-gamma globulins (Lay/Pom) with Shared idiotypic

To matti-gamma probable (Lay/Pom) with Shared idiotypic

To matti-gamma globulin (Lay/Pom) with Shared idiotypic

To matti-gamma probable (Lay/Pom) with Shared idiotypic

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To matting
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-1.
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78.6%; Pred. No. 1.6e-29;
.ive 8; Mismatches 12; Indels
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34 COMPLEMENTARITY-DETERMINING-
49 FRAMEWORK-2.
56 COMPLEMENTARITY-DETERMINING-
88 FRAMEWORK-3.
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
108
34 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
34 COMPLEMENTARITY-DETERMINING-
107 FRAMEWORK-4.
88 BY SIMILARITY.
108
34 COMPLEMENTARITY-
108
35 SIMILARITY.
KVIM_HUMAN STANDARD; PRI; 108 AA. P01665; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-I region Lay.
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Matches 88; Conserv
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August 14, 2002, 15:22:14 ; Search time 187.61 Seconds (without alignments) 219.459 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 45 summe Database : SPTREMBL_19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES			Describtion		O91wf8 mus	091ws9 mus	O9r1a5 mus	091w12 mus	091x10 mus	Ogul77 homo	Omod 996sa9 homo	Ogn170 homo		Q9ul79 homo	Omod 996pg	099m11 mus	096e61 homo	Q920e9 mus	Omod 871u90
•			10	Q99M37	Q91WF8	091WS9	Q9R1A5	Q91W12	091XL0	Q9UL77	Q96SA9	09UL70	Q9UL81	09UL79	Q96PF6	Q99M11	Q96E61	Q920E9	09UL78
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30.9	30.6	30.5	30.0	30.0	29.6	29.5	28.4	28.3	28.0	28.0	27.9	27.1	26.6	26.5	26.0	24.7	24.0	22.3	19.6	19.3	19.1	18.8	18.2	17.4	17.1	16.9	16.8
382.5	379	377	371.5	371.5	366	365	351	350	346.5	346	345	335	328.5	328	321.5	306	297	275.5	243	238.5	236.5	232	225	215	212	208.5	207.5
17	16	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Query Match 60.3%; Score 746.5; DB 11; Length 238; Best Local Similarity 58.5%; Pred. No. 1.5e-57; Matches 137; Conservative 40; Mismatches 56; Indels 1; Gaps

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Gaps

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71 LIYAASNLESGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQSNEDPRTFGQGTKVEI 130
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                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                        11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                             10 LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGI----ANYLNWYQQKPDGTVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                     59.7%; Score 738; DB 11; Length 233; 63.2%; Pred. No. 8e-57; ive 28; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1;
                                                                                                                    233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52BA205FDE995E2A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
XAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.6%; Score 725; DB 11; Best Local Similarity 63.3%; Pred. No. 9.8e-56; Matches 138; Conservative 30; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003600; Ig_like.
Interpro; IPR003606; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM0406; IGv.
PROSITE; PS002400; IG_like; 1.
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                                                                                                                                                                       Query Match
Best Local Similarity 63.29
Matches 144; Conservative
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                                                                                  Hypothetical protein.
NON_TER 1
SEQUENCE 233 AA; 2
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                      65 GQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGSHVPYTFGS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                                                     125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
                                                                                                                                                       61 QOKPGKAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
6 ILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDY-DGDSYMNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                       ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015592; AAH15292.1; -.
Hypothetical protein.
SROUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091WS9 PRELIMINARY; PRT; 233 AA.
091WS9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 25.9 KDA PROTEIN.
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60.1%; Pred. No. 6.6e-57;
Live 33; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                234 AA
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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Indels

Length 214;

RESULT Q91WS9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUB-KIDNEY;
Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                     57.0%; Score 705.5; DB 11; Length 235; 61.1%; Pred. No. 5.7e-54; ive 31; Mismatches 50; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           091XL0.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 6610010P20, FULL INSERT SEQUENCE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Ohordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina
                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006643; AAH06643.1; -. SEOUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                            091W12 PRELIMINARY; PRT; 235 cm.
091W12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:6582).
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                                                                                  211 AA.
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TISSUE-BREAST TUMOR;
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Q91W12
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MEDLINE-20499374; PUDMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Oho M., Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMN--WYQQKPGKAPKLLIYAASNLESG
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                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE-KIDNEY;
BEDLINE-21085660; PubMed-11217851;
RIKEN FANTOM CONSORTIUM.:
"Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10.1757-1771(2000).
EMBL; AK002514; BAB22154.1;
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Pred. No. 6.7e-54;
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MEDLINE-99279253; PubMed-10349636;
Carnincl P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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61.8%;
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                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934; MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson term analysis of polyreactive monoclonal antibodies from rheumatic cardits: human anti-N-acetylglucosamine/anti-myosin antibody V credion genes.";
J. Immunol. 161:2020-2031(1998).
EMBL: U96396; AAB68785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 463.5; DB 4; Length 107;
Pred. No. 3e-33;
6; Mismatches 7; Indels 5,
                                                                                                                                                                                                                                                                                                                               Score 471; DB 4; Length 108; Pred. No. 6.8e-34;
                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                     108 108
108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                              Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 19; 1.
NON_TER
  108 AA.
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                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
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                      Created)
  PRT;
                                                                                                                                                                                                                                                                                                                               38.1%;
83.0%;
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83.9%;
                     01-MAY-2000 (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                      93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.5
Best Local Similarity 83.9
Matches 94; Conservative
 PRELIMINARY;
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                                                                            Homo sapiens (Human).
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                                                                                                            NCBI_TaxID=9606;
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SEQUENCE
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SEQUENCE
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Q96SA9;
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Q96SA9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                        21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 !oung D.C.;
Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                      57 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQS-YSTLTFGGGTKVEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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MEDILINE-99277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 450; DB 4; Length 108; larity 78.6%; Pred. No. 4.7e-32; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                          01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                             81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelk
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; IREI.
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                   PRELIMINARY;
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SMART; SM00406; IGv; 1.
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108 AA;
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hes 88; Conserv
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Best Local Si
Matches 88;
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Q9UL81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                              'Myosin-reactive autoantibodies in rheumatic carditis and normal
'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                              Score 438.5; DB 4; Length 107;
Pred. No. 4.7e-31;
9; Mismatches 10; Indels 5,
                                                                                                                                                                                                                 81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.3%; Score 437; DB 4; Length 108; 77.7%; Pred. No. 6.4e-31; ive 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                        107 107
107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA; 11787 MW; DB5845F19724FB4E CRC64;
               Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF03503; AAD56269.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
NON_TER
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78.6%;
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87; Conservative
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                                                         Interracy
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                              Query Match
Best Local Similarity
Matches 88; Conserva
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Q9UL79
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81 GVPSRFSGSGSGTDFTLFISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                             MEDLINE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; contributions of organ involvement in primary systemic amyloidosis: burden."; Blood 98:714-720(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                      Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL: 9C002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
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                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
KAPPA I LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KDA PROFEIN.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%; Score 433; DB 4;
70.8%; Pred. No. 1.6e-30;
Live 14; Mismatches 17;
  116 AA.
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SMART; SM00409; 1G; 2.
SMART; SM00406; 1G: 1.
SMART; SM00406; IGv: 1.
SMART; SM00410; IG_11ke; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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PRT;
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
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Best Local Similarity 70.8%
Matches 85; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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SEQUENCE 235 AA; 2
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SEQUENCE
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Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
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SIGUELE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
Strausberg R.; 2001) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
SEMBL; BC012876; AAH12876.1; -7 FC9FB3622FED957 CRC64;
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957
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ches 86;
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Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
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CEI_TaxID=10090;
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12046 MW; 1E46988AA6858526 CRC64;
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Search completed: August 14, 2002, 15:22:14 Job time: 682 sec

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August 14, 2002, 15:15:34 ; Search time 230.21 Seconds (without alignments) 114.832 Million cell updates/sec
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Description	Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Auti-Fas humanised Humanised HFE7A de Auti-Fas humanised Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas	
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113 114 114 116 116 117 118 118 118 118 118 118 118 118 118	N N N N N N N N N N N N N N N N N N N	RESULT AAW9093

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between canti-inematic apoptosis in cells with a normal system, by inhibitic, antidiamatory, darmatological, immunosuppressive, thyromimetic, antidiateriosclerofic, cardiant and hepatropic activity. (I) induce antiarteriosclerofic, cardiant and hepatropic activity. (I) induce capoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic capoptosis by binding to cell surface Fas or inhibit it by competitive capoptosis by binding to cell surfaces, remained arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic versus host disease, Sjorgen's syndrome, coopeasture syndrome, Coopeasture, and Lingy, arterioscierosis, myocacidits, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody light chain construct designated Leu 2 hundring in the method of the invention.
                                                                                                                                                                      New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                Takahashi T;
                             Tamaki I,
                             Nakahara K,
                                                                                                                                                                                                                                                                                       Claim 2; Page 159; 263pp; English.
                             Haruyama H,
                                                                                   WPI; 2000-258930/23
                                                                                                                   N-PSDB; AAA11632
                             Serizawa N,
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238 AA; Sequence

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                         Gaps
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   Length 238;
                       Indels
   DB 21;
100.0%; Score 1237; DB 21
100.0%; Pred. No. 4.1e-60;
iive 0; Mismatches 0;
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Best Local Similarity 100.
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AAW90930 standard; Protein; 238 AA 08-AUG-2000 (first entry) AAW90930; RESULT AAW90930 NX K

Humanised anti-Fas designed light chain Leu 1 protein.

anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabates mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. human; anti-inflammatory; anti-anemic; antidiabetic; Synthetic.

EP990663-A2.

05-APR-2000

99EP-0307711. 29-SEP-1999;

98JP-0276881. 30-SEP-1998;

98JP-0276882. 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Takahashi T; Serizawa N, Haruyama H, Nakahara K, Tamaki I,

WPI; 2000-258930/23. N-PSDB; AAA11631 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 156-157; 263pp; English.

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with a normal system, by inhibiting binding between the proposition of the invention have anti-inflammatory, anti-abletic, anti-allergic, anti-arthritic, anti-inflammatory, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antilhertility, neuroprotective, antirhenmatic, nephrotropic, antilhertility, inhibit it by competitive composition of ligand binding. (I) are used to treat and/or prevent inhibit and system, especially systemic ulpus exthematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Slorgem's syndrome, pernicious or hypoplastic anemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosolerosis, myocarditis, cardiomyopathy glomerulonephitis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They aligned, do not induce liver disease, and have reduced risk of the native ligand, do not induce liver disease, and praye induced in the contractive site of Fas, i.e. they minic the native ligand, and praye and prayers, and prayers and prayers. inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody light chain construct designated Leu 1 which is described in the method of the invention. This invention describes a novel humanized anti-Fas antibody-like

238 AA; Sequence

Gaps ; 0 Length 238; Indels Score 1233; DB 21;
Pred. No. 6.7e-60;
1; Mismatches 0; 99.78; 99.68; Best Local Similarity 99.6 Matches 237; Conservative Query Match Best Local 9

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                      QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                    121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                   GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas designed light chain Leu 3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW90932 standard; Protein; 238 AA
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANY ) SANKYO CO LID.
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upose erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-mas antibody light chain construct designated Leu 3 which is described in the method of the invention.
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associated with the Fas/Fas ligand system, especially systemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis; HFE7A, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 238;
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Pred. No. 7.6e-60;
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99.2%; Pred. No. 7.be-v
2; Mismatches
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/label= Mat_protein
21..131
/label= Variable
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Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AA;
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1 metdtillwvlllwvpgstgeivltgspgtlslspgeratlsckasgsvdydgdsymnwy

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This is the amino acid sequence or the PDHH type humanised light chain of murine anti-human Peas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49K; H805, P81R, V82L, B84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coll pishH5 SANK 70398 hazboxs plasmid pHSHF5 carrying a fusion fragment of the humanised PDHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Heshimoto's disease, clarenderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant ceptcion (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the PDHH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                 Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 218; 292pp; English.
                                  44..58
/label= CDR_L1
/note= "claim 9"
                                                                                                                       /note= "claim 9"
113..121
/label= CDR_L3
/note= "claim 9"
                /label= Constant
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/label= CDR_L2
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97JP-0082953.
97JP-0169088.
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N-PSDB; AAV70077.
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01-APR-1997;
25-JUN-1997;
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                                                                                     1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDXDGDSYMNWY 60
                                              0;
    DB 19; Length 238;
                                              Indels
Query Match 95.1%; Score 1177; DB 19; Best Local Similarity 93.3%; Pred. No. 7.2e-57; Matches 222; Conservative 9; Mismatches 7;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFFTA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephiritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AABI4777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                               murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardicomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                   121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                            181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                     Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                     QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                        TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                       181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                         Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                   METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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7.2e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HFE7A designed light chain protein.
                  Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 141-142; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             AAW90927 standard; Protein; 238 AA.
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              93.38;
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                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SANY ) SANKYO CO LID.
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                Similarity
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              Local Sim
hes 222;
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus errythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Siorgen's syndrome, perntcious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoinmune hemolytic anemia, sterility, mysathenia gravis,
antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
munanised anti-Fas antibody HEFA designed light chain which is used in
the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1177; DB 21; Length 238;
Pred. No. 7.2e-57;
9; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis; HFE7A, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
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/label= Sig_peptide
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93.3%;
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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chain of murine anti-human Psayanne.

Chain of murine anti-human Psayanne.

Humanisation of the murine sequence (see AAW83042) entailed making party. W812, E84P, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coll pHsGHH7 SANK 73497 arbors plasmid pHsGHH7 carrying a fusion fragment of the human light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A apportosis in abnormal cells. The humanised antibodies special colls. The humanised antibodies in abnormal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve FasfFas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus errorm contractions and also to treat such diseases, and contractions and also to treat such diseases, including autoimmune disease getty expressions host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sjögren syndrome, pernicious anaemia, Addison's disease, rscenterederna, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, anyocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the HH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jun O, Kimihisa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 199-199; 292pp; English.
21..238
/label- Mat_protein
                                                 label≂ Variable
                                                                                    'label - Constant
                                                                                                                                          'note= "claim 9"
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                                                                                                                                                          74..80
/label- CDR_L2
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|abel= CDR_L1
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97JP-0082953.
97JP-0169088.
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/label= C
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                                                                                                                                                                                                                                                                                                                                                    30-MAR-1998;
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Protein
                                  Region
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                          QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                                                                                                         METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                  Humanised anti-Fas antibody light chain, SEQ ID NO:50.
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                                                                                                                                                                                                                                                                                                      AAB14772 standard; Protein; 238 AA
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Chimeric - Homo sapiens.
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238 AA;

Sequence

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Gaps

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Length 238; Indels

94.7%; Score 1172; DB 19; 92.9%; Pred. No. 1.3e-56; Live 9; Mismatches 8;

Conservative

Matches 221;

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Query Match Best Local &

Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                                                                   QOKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                       Gaps
                                                                            METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                  GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis selectively
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Length 238;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example reference 14; Page 114-115; 263pp; English.
   DB 21;
                                 .,
6
Score 1172; DB 21
Pred. No. 1.3e-56;
9; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells with abnormal Fas-Fas ligand systems
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 94.7%;
92.9%;
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98JP-0276882.
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            Similarity 92.9
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANY ) SANKYO CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-2000
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Query Match
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Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidabetic, anti-alergic, anti-arthritic, antiviral, immunosuduatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerctic, cardiant and hepatropic activity. (I) induce antiarteriosclerctic, cardiant and hepatropic activity. (I) induce inhibition of ligand binding (C) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                             mimic
                                                                                                                                                                                                                           disease, autoimmune hemolytic anemna, sterility, mysthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocardis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, 1.e. they mind: the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-nurine antibody response. This sequence represents a humanised anti-Fas antibody HFR7A light chain HH type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; mysthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apopticosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-Fas humanised antibody HFE7A light chain HM type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1172; DB 21
Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83032 standard; Protein; 238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 92.9
Matches 221; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
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Homo sapiens Synthetic

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Sequence
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Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
              21..238
/label- Mat_protein
Location/Qualifiers
          'label = Sig_peptide
                        1..131
label= Variable
                                   132..238
/label- Constant
                                                                      /note= "claim 9"
                                                      /note- "claim 9"
                                                                                    /note= "claim 9"
                                              44..58
/label- CDR_L1
                                                                /label- CDR_L2
                                                                          113..121
/label= CDR_L3
                                                                                                                            97JP-0276064.
97JP-0082953.
97JP-0169088.
                                                                                                                   98AU-0059701.
                                                                                                                                                 (SANY ) SANKYO CO LTD.
                                                                                                                                                           Hideyuki H,
                                                                                                                                                                         WPI; 1998-543440/47.
                                                                                                                                                                               N-PSDB; AAV70075
                                                                                                                                  01-APR-1997;
25-JUN-1997;
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Key
Peptide
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS

Claim 21; Page 200; 292pp; English.

This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFETA.

Humanisation of the murine sequence (see AAM83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coli pHSGHM17 SANK 73957 harbors plasmid pHSGHM17 carrying a fusion fragment of the humanised HM type HFETA light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA (see AAW8301-37), like native HFETA, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus erythematosus, Hashimoto's disease, cleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, atopy, arteriosclerosis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant celection (all claimed).

238 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE/A, or a humanised version of HFE/A containing identical CDRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \int
                                                                                                                                                                                                                                                                                                                                                                                                        QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                            1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                        Length 238;
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                                                                                                                                 Indels
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93.7%; Score 1159; DB 19; 92.0%; Pred. No. 6.8e-56;
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                                                                                                                       Matches 219; Conservative
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Chimeric - Homo sapiens.
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N-PSDB; AAA72125.
                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; anti-rematic; anti-res; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpurz; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                   QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                  TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                          Gaps
                                                                                                         1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody HFE7A light chain HM type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakahara K, Tamaki I, Takahashi T;
                                                    Length 238;
                                                                         Indels
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                                                    DB 21;
                                                  Score 1159; DB 21;
Pred. No. 6.8e-56;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
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                                                 93.7%;
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98JP-0276882.
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N-PSDB; AAA11563.
                                                               Similarity
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                    238
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 antibodies.
                                                                        Matches 219;
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Ingand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-alergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, pernicious or hypoplastic userius host disease, Sjorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral inhibit, apoptosis in normal cells but selectively induce it in abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEFAA light chain HM type which is used in the method described in the invention.
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
acppy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
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Pred. No. 6.8
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238 AA;

Sequence

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This is the amino acid sequence of the PDHM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chiain. Host call Escherichia coli pHSHMZ SANK 70198 harbors plasmid pHSHMZ Carrying a fusion of the humanised PDHM type HFE7A light chain and is methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells methods for inducing apoptosis in abnormal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lugus erythematosus, Hashimoto's disease, cleases, scleases, sclease, scleases, sclease, scleases, scleases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Page 220-221; 292pp; English.
                                                                                            /label= Sig_peptide
21..238
/label= Mat_protein
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                74..80
/label= CDR_L2
/note= "claim 9"
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113..121
/label CDR_L3
/note= "claim 9"
                                                                                                                                                          21..131
/label= Variable
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/label= Constant
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/label= CDR_L1
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97JP-0169088
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Masahiko O, Nobufusa
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N-PSDB; AAV70078.
Homo sapiens.
Synthetic.
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                                                                            Peptide
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                 61 QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                   121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                              Gaps
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                                                                                                                                                                                                                                                                                                            1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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            Length 238;
                                              Indels
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Score 1158; DB 19;
Pred. No. 7.7e-56;
                                             10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14778 standard; Protein; 238 AA.
            93.6%;
92.0%;
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          Query Match
Best Local Similarity 92.09
Matches 219; Conservative
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Chimeric - Homo sapiens.
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N-PSDB; AAA72177.
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 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                    OOKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                                                                                                          Length 238;
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                                                                                                                            93.6%; Score 1158; DB 21; 92.0%; Pred. No. 7.7e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HFE7A designed light chain protein #2.
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98JP-0276882.
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Best Local Similarity 92.09
Matches 219; Conservative
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 glomerulonephritis,
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                                                                           238 AA;
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30-SEP-1998;
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                                                                              Sequence
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

capoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

canti-memic, antidiabetic, anti-arthitic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antistremiosclerotic, cardiant and hepatropic activity. (I) induce

capoptosis by binding to cell surface Fas or inhibit it by competitive

inhibition of ligand binding. (I) are used to treat and/or prevent

calseases associated with the Fas/Fas ligand system, especially systemic

clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Slorgem's syndrome, pernicious or hypoplastic

cuenta, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

cardiomyopathy, glomerulonephritis, hepatlitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human and murine Fas, so can be evaluated in

cells. They bind to both human anti-murine antibody response. This sequence represents

a humanised anti-reas antibody HeFAA designed light chain which is used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
Example reference 21; Page 144-145; 263pp; English.
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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 92.0
Matches 219; Conservative
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Search completed: August 14, 2002, 15:15:35 Job time: 833 sec

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US-08-788-800-11
US-08-47-642B-40
US-09-097-309-2
US-09-097-171A-2
US-09-097-312-40
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US-09-026-985-51
US-09-026-985-72
US-09-026-985-72
US-09-026-985-72
                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
STREET: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9613152 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-Sep-95
ATTORNEY/AGENT INPORMATION:
NAME: NOTMAN D. HANSON
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
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97.78;
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Best Local Similarity
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   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 218
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RESULT
                                                                                                       August 14, 2002, 15:17:03 ; Search time 82.88 Seconds (without alignments) 70.141 Million cell updates/sec
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Compugen Ltd
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US-09-109-207C-13
US-09-296-005-13
US-09-286-163B-9
US-09-282-505-1
US-09-054-255-1
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US-08-887-3528-17
US-08-887-3528-19
US-09-109-207C-15
US-09-109-207C-17
US-09-109-207C-19
US-09-296-005-15
US-09-296-005-17
US-09-296-005-17
US-09-296-005-19
US-09-296-005-19
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US-09-296-005-19
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US-07-934-373C-39
US-08-437-642B-39
PCT-US93-07832-39
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US-08-437-642B-25
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                                                                                                                                                                                                                                                                              231628 seqs, 24425594 residues
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                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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length: 2000000000
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Query
Match Length D
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Maximum DB
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APPLICANT: Martin, Ulrich, et al. TTLE OF INVENTION: ALLI-Selectin antibodies for prevention of multiple organ f NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1108; DB 5;
Pred. No. 1.6e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
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121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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APPLICANT:
APPLICANT:
Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITT: South San Francisco
STREET: California
COUNTRY: USA
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                                    DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                        81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF
                                                                                                                                                                                141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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 2; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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Pred. No. 1.7e-86;
                                                                                                                                                                                                                                                         201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                            3; Mismatches
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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Best Local Similarity 97.2%;
Matches 212; Conservative
 Conservative
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US-08-887-352B-13
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Matches 213;
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                        STREET: JUNA WAY
CITY: South San Francisco
STREET: Alifornia
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PSTREM: PC-DOS/MS-DOS
                        201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/466,151
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/18589
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/874768
FILING DATE: 14-AUG-1991
ATTORNEY/AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                            Sequence 9, Application US/08466151 Patent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                              Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                           US-08-466-151-9
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81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                 Length 218;
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
                                                                                                                                                 Score 1096; DB 4; Length 2
Pred. No. 1.7e-86;
3; Mismatches 3; Indels
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88.6%; Score 1096; DB 4;
Best Local Similarity 97.2%; Pred. No. 1.7e-86;
Matches 212; Conservative 3; Mismatches 3;
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; Patent No. 6329509
; GENERAL INFORMATION:
    APPLICANT: Jardieu, Paula M.
    APPLICANT: Jardieu, Paula M.
    TITLE OF INVENTION: Immunoglobulin Variants
    FILE REFERENCE: P0718PZC1D1
    CURRENT APPLICATION NUMBER: US/08/466,163B
    CURRENT FILING DATE: 1995-06-06
    PRIOR APPLICATION NUMBER: US 08/405,617
    PRIOR APPLICATION NUMBER: US 08/185,899
    PRIOR FILING DATE: 1995-03-15
    PRIOR FILING DATE: 1995-03-15
    PRIOR FILING DATE: 1994-01-26
; PRIOR FILING DATE: 1997-05-07
; PRIOR FILING DATE: 1997-05-07
; PRIOR FILING DATE: 1991-08-14
                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                 Query Match 88.6%;
Best Local Similarity 97.2%;
Matches 212; Conservative
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US-08-466-163B-9
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LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 13
LENGTH: 218
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   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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LOCATION: 1-218
CTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13
                                                                                                                 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09109207C
Patent No. 6172213
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Patent No. 6290957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial FEATURE:
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FEATURE:
NAME/KEY: Artificial
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US-08-887-3528-24
US-08-887-3528-24
Sequence 24, Application US/08887352B
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Pred. No. 2.9e-84;
6; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                3: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Winderin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-7u1-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFRENCE/CDOCKET NUMBER: 91123
TELECOMMUNICATION NUMBER: 91123
TELECOMMUNICATION NUMBER: 91123
TELECOMMUNICATION NUMBER: 91123
TELECOMMUNICATION NUMBER: 91123
TELEPHONE: 650/252-1489
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                          ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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95.0%;
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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Amino Acid
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Best Local Similarity 95.09
Matches 207; Conservative
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    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS: ADDRESSE: Genetech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: California
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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Pred. No. 2.9e-84;
6; Mismatches 5;
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181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELEPHONE: 650/225-1489
TELEPHONE: 650/952-9881
                                                                                                                                                                                        Sequence 17, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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Best Local Similarity 95.08
Matches 207; Conservative
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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US-08-887-352B-17
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
TITLE OF INVENTION INDIVIDED: 191231
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION UNBER: US 60/051,554
PRIOR PILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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                     61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
                                                                                                                                               Gaps
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95.0%; Pred. No. 2.9e-84;
iive 6; Mismatches 5;
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US-09-109-207C-19
Sequence 19, Application US/09109207C
Patent No. 6172313
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Matches 207; Conservative
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SEQ ID NO 17
LENGTH: 218
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ORGANISM: Artificial
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NAME/KEY: Artificial
LOCATION: 1-218
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APPLICANT: Henry B
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US-09-109-207C-17
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LENGTH: 218
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Patent No. 6172213
GENERAL INFORMATION:
GENERAL APPLICATION NUMBER:
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. OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 2.9e-84;
6; Mismatches 5;
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Pred. No. 2.9e-84;
6; Mismatches 5;
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....ек: US/OB/887,352B
03-Jul-1997
03-Jul: 530
                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112:
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/255-1489
TELEPHONE: 650/255-1489
                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
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95.0%;
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95.0%;
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Best Local Similarity 95.0%
Matches 207; Conservative
                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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US-08-887-352B-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Artificial
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Matches 207; Conserv
                                                                             FILING DATE:
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US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                        1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 60
; ORGANISM: Artificial
; FEATURE:
; NAME/KET: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
                                                                                                                                               ;
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                                                                                                                Query Match

86.5%; Score 1070; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                          STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq kappa chain NIG	Kappa	kappa chain	chain	Ig kappa chain Am3	Ig kappa chain pre	kappa chain	Ig kappa chain - s	Ig kappa chain pre	noclonal anti	kappa	kappa chain	kappa	kappa chain		kappa chain	Ig kappa chain - m		kappa	kappa chain			kappa chain	kappa chain		kappa	kappa chain	lambda-like	kappa chain
SUMMARIES	QI	JE0242	JE0244	JE0243	A23746	JE0241	S06084	S68241	S33161	S14237	JC5810	A31790	S01320	A56169	S37484	PC4203	S52028	S38865	S25058	S68212	S42772	S16112	JL0029	A20969	PT0219	S52059	S29593	PH1226	A49633	PL0106
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dЬ	Query Match Length		75.2	73.4	71.9	71.2	65.7	6.09	8.09	8.09	60.7	59.0	58.6	58.4	58.2	57.7	57.2	57.1	57.1	56.7		55.9						47.1		
	Score	949.5	930.5	907.5	889.5	881	813	753	752.5	752	751	730	725	722	720.5	713.5	707.5	706.5	706.5	701	697.5	691.5	680.5	617.5	612	608.5	586.5	583	572.5	551
	Result No.	1	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

31   516   44.3   106   1   K3HU   10   1   K9896   33   433   433   131   1   KW886   19   48ppe   33   536   433   131   1   KW886   19   48ppe   33   536   43.3   131   1   KW886   19   48ppe   34   518   41.9   132   2   540367   19   48ppe   35   514   41.9   132   2   540367   19   48ppe   35   514   41.9   11.2   2   540367   19   48ppe   35   514   41.9   41.2   437927   19   48ppe   36   514   41.0   11.2   43.7927   19   48ppe   42   503   40.1   10   42   503   503   40.1   10   42   503   504   40.1   10   5   5   5   5   5   5   5   5   5	Ig kappa chain Cr Ig kappa chain pre Ig kappa chain pre Ig light chain - r Ig kappa chain - h Ig kappa chain V-J Ig kappa chain V-I Ig kappa chain Cr Ig kappa chain Pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain - h Ig light chain pre Ig kappa chain - h Ig light chain pre Ig kappa chain - h Ig kappa chain - h	ALIGNMENTS	05-Dec-1998 #text_change 21-Jan-2000 ; Takeda, K.; Kojima, M.; Takashi, I.; Shinoca f kappatype light chains with AL amyloidosis: immunoglobulin homology	Gap	DYDGDSYMNWYQQRPGQAPKLLIYAASNLES 80 :: :                  - SNNYLAWYQQRPGQAPSLLIYDASSRAT 57	GVPSRFSGSGSGTDFTLISSLOPEDFATYXCQOSNEDPRTFGQGTKVEIKRTVAAPSVF 140  :                    :             :	FPPSDEQLKSGTASYVCLLNNFYPREAKVQMKVDNALQSGNSQESYTEQDSKDSTYSLS 200 	KSENRGEC 238           KSENRGEC 215	<pre>i5-Dec-1998 #text_change 21-Jan-2000 'akeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H light chains (VkV) identified in cases of AL immunoglobulin homology</pre>
30 548 44.3 106 1 31 536 43.3 131 1 32 521 42.1 132 1 33 520 42.0 233 2 34 518 41.9 123 3 36 514 41.8 127 2 37 513 41.9 123 2 38 514 41.6 141 2 39 509.5 41.2 145 2 41 509.5 41.2 145 2 42 509 41.1 140 2 42 509 41.0 139 2 43 509 40.3 132 2 44 499 40.3 132 2 44 499 40.3 132 2 45 Alim, M.A.; Yamaki, S.; Hossain Submitted to JIPIO, November 199 A; Description: Structure relation A; Reference number: JBC241 A; Residues: 1-1216 ALID: C; Superfamily: immunoglobulin b A; Residues: 1-1216 ALID: C; Superfamily: immunoglobulin b Best Local Similarity 81.9%; Matches 183; Conservative C; Superfamily: immunoglobulin b F; 16-91/Domain: immunoglobulin b F; 16-9	K3HU KVMS32 S29577 S40331 S40134 A49134 A37927 S20633 S20633 S20633 S20633 S20633 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2033 S2	ALIG	human vision ( n, M.S.; B nship of nship of	Score Pred. 14; Mis	CKASQSVI  :      CRASQSV-	PEDFATY :       EPEDFAVY	FYPREAKV                 FYPREAKV	GLSSPV7	0
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215;

Length

DB 2;

homology

1mmunoglobulin

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C; Accession: JE0241
R; Alm, M. B.; Yamaki, S.; Hossaln, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998
A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JE0241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-216 <ALI.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 881; DB 2; ilarity 80.3%; Pred. No. 1.2e-50; Conservative 14; Mismatches 27
                                                                                                                                                  Score 889.5; DB 2
Pred. No. 3.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-215 < LEO>
C, Superfamily: immunoglobulin V region; immuno
C, Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                       13;
                                                                                                                                                  71.9%;
                                                                                                                                                  Query Match
Best Local Similarity 82.09
Matches 178; Conservative
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Ig kappa chain Am37 precursor
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Matches 175; Conserv
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C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0243
B; Ail m. A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Submitted to JIPID, November 1998
A; Description: A new subgroup of k type light chains (VkV) identified in cas A; Reference number: JE0243
A; Accession: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Till KAU cold agglutinin) - human C; Species: Homo sapiens (man) C; Species: Hext_change 21-Jan-2000 C; Accession: A23746 R; Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B. J. Biol. Chem. 266, 2836-2842, 1991 A; Title: The primary structure of the Fab fragment of protein KAU, a monocle A; Reference number: A23746; MUID: 91131575
                                                                                                                                                                                                                           140 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNEDPRTFGQGTKVEIK-RTVAAPSV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 199
                                                                                              Gaps
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                                                                                                                                                    DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                                                                                                                        81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNE-DPRTFGQGTKVEIKRTVAAPSV
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                                                         Length
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<IMM>
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                                                      Score 930.5; DB 2;
Pred. No. 7.2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.4%; Score 907.5; DB 2
82.2%; Pred. No. 2.3e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Molecule type: protein
A Mesidues: 1-215 CALIS
C;Superfamily: immunoglobulin V region;
F;16-90/Domain: immunoglobulin homology
F;16-90/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain NIG93 precursor - human
                                                                                          13;
                                                      75.2%;
83.6%;
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Best Local Similarity 82.23
Matches 180; Conservative
                                                                                        Matches 183; Conservative
                                                                         Similarity
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5

Gaps

7

Indels

27;

Length 216;

80 58

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Ig kappa chain precursor (15C5) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: 514237 R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D. Bur. J. Biochem. 192, 767-775, 1990 A;Title: Construction and characterization of a recombinant murine monoclonal antibod A;Reference number: 514236; MUID:91006173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1990
A; Description: Isolation and characterisation of sheep kappa light chain cDNA.
A; Reference number: S33161
                                                                                                                                                                                                                                                                                                                                                                                   (domestic sheep)
#text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology F;143-212/Domain: immunoglobulin homology <IMM>
       58 QAPKLLIYYATRLHTDVPSRFSGSGSGTDYTLTISNLEANDTATYYCLQYESTPLAFGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623 (S. Superfamilly: Immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
                                                                               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLWVLLLW-VPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 SVIEQDSKDSIYSLSSTLILSKADYEKHKVYACEVIHQGLSSPVIKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 230;
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3e-42;
ches 47;
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                                                                                                                                                                                                                                                                                                                                                                              C.Species: Ovis orientalis aries, Ovis ammon aries C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C.Accession: S33161 R.Foley, R.C.; Beh, K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%; Scor.
62.7%; Pred. No. oc.
''ve 35; Mismatches
                                                                                                                                                                                                         STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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Best Local Similarity 62.73
Matches 146; Conservative
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A; Molecule type: mRNA
A; Residues: 1-230 <FOL>
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N.Alternate names: immunoglobulin light chain
C.Species: Mus musculus (house mouse)
C.Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: 568241; S68242
R.; Handan, A.; Handan, A.; Yamaguchi, H.; Kamachi, M.; Immanka, T. submitted to the EMBL Data Library, March 1994
A; Reference number: 568241
A; Reference number: 568241
A; Molecule type: mRNA
A; Residues: 1-218 < TANA
A; Residues: 1-218 < TANA
A; Residues: 1-218 < TANA
A; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FEBS Left. 375, 273-276, 1995
A; Taltle: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A; Reference number: 568211; MUID: 96085223
A; Rolecule type: mRNA
A; Reference number: 568211; MUID: 96085223
A; Molecule type: mRNA
A; References nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 'Un', 3-212 < TANA
A; Residues: EMBL: D29570
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                      rat myeloma immunoglobulin kappa chain cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 WYQQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 PRIFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                       A; Accession: S06084
A; Accession: S06084
A; Mesidues: 1-240 CCRO>
A; Cross references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 1-240/Product: Ig kappa chain #status predicted <MAT>
F; 153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGD--SYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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Pred. No. 2.6e-42;
0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                        65.7%; Score 813; DB 2;
65.0%; Pred. No. 3.6e-46;
tive 30; Mismatches 52
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3.
A;Reference number: S06084; MUID:90016888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.9%; Scc
64.7%; Pre
tive 30;
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similaria,
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.9
Best Local Similarity 64.7
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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65

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Gaps

5

Indels

49;

Score 730; DB 2; Pred. No. 8.3e-41;

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin di A; Reference number: S01320
A; Molecule type: MRNA
A; Residues: 1-234 cDEL>
A; Accession: S01320
A; Molecule type: MRNA
A; Residues: 1-234 cDEL>
A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
A; Note: this sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-234/Product: Ig kappa chain #status predicted <AMT>
F; 36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198
                                                                                                                                                                                                                                                                                                   21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDG--DSYMNWYQQKPGQAPKLLIYAASNL 78
                                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGVPSRFSGSGSGTDFTLT1SSLQPEDFATYYCQQSNEDPRTFGQGTKVE1KRTVAAPS
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.0%; Score 730; DB Best Local Similarity 62.3%; Pred. No. 8.3e-Matches 137; Conservative 32; Mismatches
                                  C; Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody 13-1 light chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C; Accession: JC5810
R; Akashi, S; Kato, K; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A; Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A; Reference number: JC5810; MUID:98063277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an
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                                                                                                                                                                                                                              61 QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                        121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                            GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                 9
                                                                                                                                                            1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCKASQDI----NSYLSWI 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                  Indels
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Pred. No. 3.3e-42;
; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Pred. No. 3.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
                               35;
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65.18;
60.1%;
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Best Local Similarity 60.1
Matches 143; Conservative
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mouse recombinant immunoglobulin directe

59 WYQQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNED 118 Gaps 54 1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMN--119 PRIFGQGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC Length 234; - mouse (fragment) 55; Query Match
58.6%; Score 725; DB 2;
Best Local Similarity 57.9%; Pred. No. 1.9e-40;
Matches 139; Conservative 38; Mismatches 55 Ig kappa chain V region (clone 23.2) -C;Species: Mus musculus (house mouse)

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us-09-499-662-129.rpr

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C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C; Accession: PC4203
R; Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A; Title: Cloning and characterization of cDNAs coding for heavy and light chains
A; Reference number: PC4203
A; Reference number: PC4203
A; Reference number: PC4203
A; Residues: 1-219 < KWA>
                                                              Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Matches 132;
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000 C;Accession: A56169
R;Monfardini, C.; Réber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
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A;Accession: A56169 MUID:95204454
A;Recule type: mRNA
A;Residues: 1-210 <ANN>
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain - mouse (fragment)
C.Species: Mis musculus (house mouse)
C.Species: Mis musculus (house mouse)
C.Species: Nis musculus (house mouse)
C.Accession: S37484
R.Pucancel, F.F.D.
A.Reference number: S37483
A.Reference number: S37483
A.Accession: S37484
A.Status: preliminary
A.Nolecule type: mRNA
A.Residues: 1-225 < DUC>
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C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
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65.6%; Pred. No. 2.6e-40;
iive 27; Mismatches 45; Indels
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A; Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-dersi
C; Superfamily: immunoglobulin v region; immunoglobulin homology
F; 1-112/Domain: V region #status predicted <VRG>
F; 113-219/Domain: C region #status predicted <CRG>
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60.3%; Pred. No. 9.7e-40;
Live 36; Mismatches 50;
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21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last annotation update) 11-JUL-1986 (Rel. 01, Last annotation update) 11-JUL-1986 (Rel. 01, Last annotation update) 11-CCT-2001 (Rel. 01, Last annotation update) 11-CCT-2001 (Rel. 01, Last annotation update) 12-SEQUENCE (MELOAD FORDIN ED) 12 ENKATYOELS MELEZOA (Chordata; Catarrhini; Hominidae; Homo. 11 Indec. 11	1834;  1834;  1834;  1834;  1834;  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  1849,  18	HUMAN KAC_HUMAN	STANDARD;	PRT;	106 AA.	
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KV3F_MOUSE
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
                                               Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
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                                                                                                                                                                     Science 169:56-59(1970).
-1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain VII region MOPC 63 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                          SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDLINE=70201507; PubMed=5447531;
KOhler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FIIGAVAR.003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

51984DIFDD372CE8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
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                       SEQUENCE (BENCE-JONES PROTEIN AG). MEDLINE-69234734; Pubmed-4893682;
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57 E
11609 MW;
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PPOATTE: PS00290; IG_MHC; 1.
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InterPro; IPR003597; Ig_c1.
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106
83
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HSSP; P01842; 7FAB.
MIM; 147200; -.
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83
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P01661;
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KV31_MOUSE
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MEDINE-79012520; PubMed-99744;
MEDINE-79012520; PubMed-99744;
MCKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR: A01935; KWSM6.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam: PF00047; ig; 11.
SMART; SM00406; IGV: 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region MOPC 321 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherias; Rodentia; Sciurognathi; Murinae; Mus. NCBI_TaxID=10090;
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MEDLINE=73140225; PubMed-4691517;
MCKean D.T., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                            Burstein Y., Schechter I.; ^{\circ} Primary structures of N-terminal extra peptide segments linked
                                                                               the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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MEDLINE=78235887; PubMed=98179;
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                                                              HSSP: A01937; KVMS43.
HSSP: P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR0047; ig; 1.
Immunoglobulin V region.
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DOMAIN 24 39 53 CC
DOMAIN 54 60 CC
DOMAIN 55 101 CC
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P01666;
21-JUL-1986 (Rel. 01, Created)
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                                     diversity.";
Nature 276:785-790(1978).
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KV3N_MOUSE
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                                                                                                                                                                                                                                                     Biochemistry 12:749-759(1973).
-!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
              SEQUENCE OF 1-37.

MEDLINE-78238887; PubMed-98179;

Burstein Y., Schechter I.;

Primary structures of N-terminal extra peptide segments linked in the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";

Biochemistry 17:2392-2400(1978).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7043.
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MEDLINE=73140224; PubMed=4120629;
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MEDLINE=79073152; PubMed=103003;
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HSSP: P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
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nes 90; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 2e-32;
9; Mismatches 11; Indels
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12002 MW; 7A5FCB586C306D29 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7183.
Mas musculus (Mouse).
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BY SIMILARITY
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Nature 276:785-790(1978).
PIR; E01937; KVMS69.
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sapiens (Human)
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129 AA;
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Matches 92; Conserv
                                   NCBI_TaxID=9606;
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P01669;
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                                                                   1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                              61 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQOSNEDPLTFGAGTKLELK 111
                                                                                                   81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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         Length 111;
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FRAMEWORK - 2.
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                                 11; Indels
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        39.2%; Score 485; DB 1;
81.1%; Pred. No. 2.8e-32;
ive 10; Mismatches 11;
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                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 6308.
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9; Mismatches
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PIR: C01937, KVMSO8.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV; 1.
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81.1%;
                               90; Conservative
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KV30_MOUSE
ID KV30_MOUSE
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                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i. DISBASE: THE PROPEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG KAPPA CHAIN V-III REGION HAH.
FRAMEMOKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWOKK-2.
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COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
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14073 MW; D3C55292772774D0 CRC64;
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ilarity 69.7%; Pred. No. 5.4e-32;
Conservative 16; Mismatches 21;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7769.
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HSSP, POLT98; LINCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pram; PP00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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P01664;
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Best Local S:
Matches 96;
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AdG-1987 (Rel. 05, Created)
13-AdG-1987 (Rel. 05, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
15-JUJ-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Walker precursor.
19 kappa chain X-I region Walker precursor.
19 kappa chain Y-I region Walker precursor.
19 kappa chain Y-I region Walker precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.8%; Score 480; DB 1; Length 111; 80.2%; Pred. No. 7.1e-32; Live 11; Mismatches 11; Indels
                                                                                                                      COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-1
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PIRS, A01883; KIHUWK.
HSSP, P01607, 1REI.
INTERPRO; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffan, PF00047; 149; 1.
Immunoglobulin V region; Signal.
SIGNAL
DOMAIN 23 129 IG KAPPA
DOMAIN 23 45 COMPLEME
DOMAIN 46 56 COMPLEME
DOMAIN 77 71 FRAMEWOR
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HSSP; P01789; 1MCP.
InterPro; IPR001006; Ig_MHC.
InterPro; IPR001596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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Best Local Similarity 80.28
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MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR, A01936; KWSC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
From Product Sci. Communication of the communication of the
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region CBPC 101.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Murinae; Musinae; Musin
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                                                       COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 129;
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FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                      MW; F941FA07D4AFC2F9 CRC64;
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Pred. No. 3.1e-31;
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Pred. No. 1.8e-31;
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            FRAMEWORK-3.
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73.3%;
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79.3%;
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129
129 AA;
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                                                       LEUKEMIA.
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SEQUENCE
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MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated Kappa 149th chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic
                                                                                                        21-JUL-1986 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region PC 7210.
Mus musculus (Mouse).
Musculus (Mouse).
Musmualia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
Musmualia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaina; Puteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              MEDELINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 462.5; DB 1; Length 110; 79.3%; Pred. No. 1.7e-30;
81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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COMPLEMENTARITY-DETERMINING-2.
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38 COMPLEMENTARITY-DETERMINING-
53 FRAMEWORK-2.
60 COMPLEMENTARITY-DETERMINING-
92 FRAMEWORK-3.
110 COMPLEMENTARITY-DETERMINING-
110 FRAMEWORK-4.
92 BY SIMILARITY.
11050 MW; 69F1A5CE886B1249 CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-III region HIC precursor.
Homo sapiens (Human).
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PIR: D01937; KVMMIO.
HSSP: P01789: IMPP.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam: PP00047; 19: 1.
SMART; SM00406; IGv: 1.
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QQKPGQAPKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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mutation. Implications for etiology and immunotherapy.";
J. EXP. Med. 167:840-852(1988).
-!- DISEASE: THE PROFILI IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin
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                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 129;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING - 2.
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Hau.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA.
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                                                                                                   PIR; PLO021; K3HUHI.
HSSP; P01789; 1MCP.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
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129
109
129
14070 M
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1;

14966 MW; 6413A22FD0738832 CRC64;

BY SIMILARITY.

us-09-499-662-129.rsp

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43
134
134 AA;
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                                                                                                                                                                                  131 EIKR 134
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Best Local Simi
Matches 88;
  DISULFID
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                                                                                                                             Gaps
                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86041854; PubMed-2997713;
Marsh P., Mills F., Gould H.;
Defection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                 Ig kappa chain V-IV region B17 precursor.

Memo saptens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                             4;
                                                                                                                                                                                  81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-IV REGION B17
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                    COMPLEMENTARITY - DETERMINING - 2.
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                                    COMPLEMENTARITY - DETERMINING - 3.
                                                                                                         Length 108;
                                                                                                      36.9%; Score 457; DB 1; Length 10;
79.5%; Pred. No. 4.7e-30;
.ive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                           08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                     134 AA
                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK - 4
                                               FRAMEWORK-4
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                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 13:6531-6544(1985).
                                                                                                                                                                                                                                                    PRT;
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HSSP; P01789; IMCP.
InterPro; IPR003306; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                           11671 MW;
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                                                                                                                          89; Conservative
                                                                                                                                                                                                                                                     STANDARD;
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P06314;
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KV4C_HUMAN
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--- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-II KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR; A01871; KIHULY.

HSSP: PO1807; IREI.

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                       69 KLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKV 128
                                                                                                                                                                                                               11 KLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQGTKV 130
                                                  Gaps
                                                                                                                   11 LLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGD--SYMNWYQQKPGQAP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra J.D., Klapper D.G.;
"Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                ;;
36.5%; Score 452; DB 1; Length 134; llarity 71.8%; Pred. No. 1.5e-29; Conservative 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING - 1.
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Pred. No. 2e-29;
8; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-I region Lay.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
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MEDLINE-77038198; Pubmed-824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                           KV1M_HUMAN STANDARD; E
P01605;
21-JUL-1986 (Rel. 01, Created)
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illarity 78.6%;
Conservative E
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SMART; SM00406; IGv; i.
Immunoglobulin V region
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Query Match
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Matches 89; Conserv
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Search completed: August 14, 2002, 15:23:13 Job time: 686 sec

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Q9u183 homo sapien
Q911812 m adult mal
Q9u186 homo sapien
Q9u185 homo sapien
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Q96jd2 homo sapien
Q96jd0 homo sapien
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 26.3 KDA PROTEIN.
HIS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscull_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.7%; Score 750.5; DB 11; Length 238; ilarity 59.0%; Pred. No. 1e-57; Conservative 39; Mismatches 56; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL.
BOTO 2035; AAH02035.1; -.
EMBL.
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   096169
091183
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                                                                                                                                                                                                                                                                                                                                                                                       1 METDTILLEWVLLLEWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q99M11
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                                           65 GQSPKLLIYKVSNRFSGVPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQGSHVPYFFGS 124
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64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S VRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQXP
                                                                  125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                          6 ILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDY-DGDSYMNWYQQKP
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                               ; Score 739; DB 11; Length 2;
; Pred. No. 1e-56;
33; Mismatches 58; Indels
                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292; AAH15292.1; -
                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOE6EB7812D2 CRC64;
                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                               59.7%;
60.1%;
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Best Local Similarity 60.1%
Matches 143; Conservative
                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-COLON;
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ 190
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilde K.G., Yu., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoc antibody (MaD 7, its light and heavy chains) and construction of single chain antibody (ScFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AR152371, AAD40242.1;
HSSP, P01679, 2FBJ.
InterPro; IPR003600; Ig_like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_WC.
Pfam; PP00047; ig; 2.
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                                                                                                                                                                          Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKŞFNRNEC 233
                                                                                                                                                                                                                        Indels
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                            233 AA; 25781 MW; B1C184DA149A16EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                            Score 738; DB 11;
Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 721; DB 11;
Pred. No. 3.3e-55;
                                                                                                                                                            59.7%; Scor.
63.2%; Pred. No. ...
144 28; Mismatches
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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23922 MW;
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62.8%;
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                                                                                                                                                                                                                        Matches 144; Conservative
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                                                              Hypothetical protein.
NON_TER 1
SEQUENCE 233 AA; 2
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214 AA;
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Best Local Similarity
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Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                     FROM N.A.
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                                                                                                    SEQUENCE
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LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAP 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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STRAIN=C57BL/6J; TISSUE-KIDNEY;
Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091XLD;
091XLD;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLOME: 0610010P20, FULL INSERT SEQUENCE.
MAS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                  57.0%; Score 705.5; DB 11; Length 235; 61.1%; Pred. No. 8.5e-54; ive 31; Mismatches 50; Indels 5;
                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006643; AAH06643.1; -. SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                                 091W12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:6582).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                211 AA.
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                                                                                                                                          PRELIMINARY;
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TISSUE=BREAST TUMOR;
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STRAINE-20499374; PubMed-11042159;
MEDLINE-20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Toshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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XX MEDLINE-20530913; PubMed=11076861;
XA Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
XA Shibata K., Itch M., Alzawa K., Kitsunai T., Tashiro H., Itch M.,
Xamanch H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Xumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Xamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1711(2000).
REBEL: AKO02514: BAB22154.1:
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"Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 2.2e-53;
3; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINE-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-99279253; Pubmed-10349636;
Carnline P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
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DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                    Created)
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                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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                                                                                                                                             PRELIMINARY;
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NON_TER
SEQUENCE
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Q9UL70
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapións (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-NYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
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MEDINE-98375893; PubMed=9712075;
MEDINE-98375893; PubMed=9712075;
Moderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis; human anti-N-acetylglucosamine/anti-myosin antibody V region genes.;
J. Immunol. 161:2020-2031(1998).
EMBL: U96396; AAB68785.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.1%; Score 459.5; DB 4; Length 107; 83.0%; Pred. No. 8.8e-33; Live 7; Mismatches 7; Indels 5
                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                             Score 467; DB 4; Length 108;
Pred. No. 2e-33;
                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                             108 108
108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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                                                                                                                                                                                                               Ciln. Immunol. Immunopathol. 87:184-192(1998).
EMBL; ARD36073.1; -.
INTEXP. POLGO7; IREI.
INTEXPO: IPRO03006; Ig_MHC.
INTEXPO: IPRO03596; Ig_V.
INTEXPO: IPRO047; 19; 1.
SMART; SMO0406; IGV; 1.
108 AA
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PRT;
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82.1%;
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PRELIMINARY;
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                    NCBI_TaxID=9606;
                                                                     (FRAGMENT)
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SEQUENCE
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NON_TER
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                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         Query Match 36.1%; Score 446; DB 4; Length 108; Best Local Similarity 77.7%; Pred. No. 1.3e-31; Matches 87; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR00047; ig; 1.
NON_TER.
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Q99M11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES 80
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21361171; PubMed-11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                 35.1%; Score 434.5; DB 4; Length 107; 77.7%; Pred. No. 1.3e-30; Live 10; Mismatches 10; Indels 5;
                                                                                                                                                                                                             81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                     35.1%; Score 434; DB 4; Length 116; 70.8%; Pred. No. 1.6e-30; tive 14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 116
116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
                                                                                                       107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA 1 LIGHT CHAIN VARIABLE RECION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
                Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                               116 AA
                                                                                                                                                                                                                                                                               PRT;
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EMBL; AF361758; AAK51465.1; -.
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                             107
                                                                                                                                         1 Similarity
87; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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01-MAY-2000 (
01-MAY-2000 (
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NON_TER
SEQUENCE
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SEQUENCE
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Q9UL79
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096PF6
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Matches
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 433; DB 4; Length 108;
Pred. No. 1.8e-30;
8; Mismatches 14; Indels
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; P01703; JrAB.
Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.
Interpro; IPR003609; Ig.like.
Interpro; IPR003609; Ig.like.
Interpro; IPR003609; Ig.like.
Interpro; IPR003609; Ig.like.
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SWART: SMO0409: 1G; 2.
SMART: SMO0406: 1G: 1.
SWART: SMO0406: 1G' 1.
SWART: SMO0410: 1G_like; 2.
PROSITE: PS00290: IG_MHC; UNKNOWN_1.
HYPOTHELIA | protein.
SEQUENCE 235 AA: 25403 MW; 39807BFE6782A3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; 1REI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.0%;
ilarity 76.8%;
Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                              Homo sapiens (Human)
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Matches 86; Conserv
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                                                                                                                         125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                 67 APKLLIYAASNLESGVPSRFSGS--GSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 APKVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 APKLLIYAASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ - QSNEDPRTFGQ 124
                                             7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQ 66
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGQ 66
                                                                                                                                                                                                                          184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                          180 QGVETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 -VETTKPSKQSNNKYAASSYLSLIPPEQWKSHRSYSCQVTHEG--SIVEKTVAPTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7%; Score 429; DB 4; Length 236;
42.4%; Pred. No. 1.1e-29;
live 39; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12876.1; -.
24712 MW; 7EC9FB3622FED957 CRC64;
                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:17259).
Homo sapiens (Human).
   Pred. No. 8.3e-30;
7; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AA.
               37; Mismatches
                                                                                                                                                                                                                                                                                                                                 PRT;
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42.68;
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Matches 100; Conservative
 Local Similarity 42.6 ses 101; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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 Best Loca
Matches
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2. SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
3. SIDSI/gcgdata/hold-geneseqy-embl/AA1982.DAT:*
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5. SIDSI/gcgdata/hold-geneseqy-embl/AA1983.DAT:*
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6. SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:*
7. SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:*
8. SIDSI/gcgdata/hold-geneseqy-embl/AA1987.DAT:*
9. SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
10. SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
11. SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
12. SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
13. SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
14. SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
14. SIDSI/gcgdata/hold-geneseqy-embl/AA1993.DAT:*
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1237
1 METDIILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum I
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:

***	Description	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	ID	AAW90932	AAW90930	AAW90931	AAW83034	AAB14777	AAW90927	AAW83031	AAB14772	AAW90922	AAW83032	AAB14773
	DB	21	21	21	19	21	21	19	21	21	19	21
	å Query Match Length DB	238	238	238	238	238	238	238	238	238	238	238
	% Query Match	100.0	6.66	99.66	94.9	94.9	94.9	94.5	94.5	94.5	93.5	93.5
	Score	1237	1236	1232	1174	1174	1174	1169	1169	1169	1156	1156
	Result No.	П	7	e	4	S	9	7	æ	6	10	11

(SANY ) SANKYO CO LTD.

Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-L-s	Mus musculus anti-	Light chain amino	Full variable ligh	Humanised MaE11 Ve	anti-	Mus musculus anti-	Mus musculus anti-	Amino acid sequenc	E27 anti-IgE antib	Mus musculus anti-	Mus musculus anti-	•	length	다	1ig	Variable light cha	Human IGFAM-10 imm	Human IGFAM-1 immu	Human immune respo	Sequence of the ka	Human reshaped F19	Human IGFAM-13 imm	Human anti-RSV mon	d se	Humanised 5G1.1 VL	pH52-9.0 humanised
AAW9092	AAW83035		AAW90928	AAW83033	AAB14774	AAW90924			AAY85200				AAW95660	AAW95662	AAB07472	AAB74211	AAW95669	-	AAB47087	AAB76949	AAB76951	-	AAB76958		AAY96289	AAB82912	AAR38162	AAY50161		AAW11638	AAG63665		AAR30777
œ	m	238 21	œ	m	m	œ	m	m	ന	m	œ	æ	ഹ		m	œ	m												237 21			236 16	233 14
93.5	93.4	93.4	93.4	93.3	93.3	93.3	0.06	88.8	88.8	88.8	88.3	87.0	87.0	87.0	87.0	87.0	86.7	86.7	86.7	86.7	86.7	86.7	86.7	85.1	84.8	84.6	84.4	84.3	84.1	84.0	82.9	82.6	
1156	1155	1155	1155	1154	1154	1154	1113	1099	1099	1099	1092	1076	1076	1076	1076	1076	1073	1073	1073	1073	1073	1073	1073	1052.5	1048.5	1046.5	1044.5	1043	1040.5	1039	1026	1022	1021.5
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized, apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                            Humanised anti-Fas designed light chain Leu 3 protein.
                              AAW90932 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0276881.
98JP-0276882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99EP-0307711.
                                                                                               (first entry)
                                                                                               08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1999;
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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2000
                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                             AAW90932;
RESULT
AAW90932
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Eas anoticis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, cantiantenic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antitrheumatic, nephrotropic, antilnfertility, neuroprotective, antistrefucelerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent disease associated with the Fas/Fas ligand system, especially systemic capptosis by binding to cell surface Fas or inhibit it by competitive computed in thibition of ligand binding. (I) are used to treat and/or prevent disease, solorgen's syndrome, pernicious or hypoplastic versus host disease, soleroderma, Goodpasture syndrome, Crompasture syndrome, Computed and System, capped and System, and is a sease, soleroderma, sterility, myssthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin disease, autoimmune hemolytic anemia, sterility, myssthenia gravis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic, and transplant rejection. (I) selectively cells in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, 1.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody reponse. This sequence represents way was antibody light construction.
                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                           Takahashi T;
                              Tamaki I,
                           Nakahara K,
                                                                                                                                                                                                                                                                                    Claim 3; Page 161-162; 263pp; English.
                              Haruyama H,
                                                                                 WPI; 2000-258930/23.
                                                                                                               N-PSDB; AAA11633
                              Serizawa N,
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Gaps ö Length 238; 0; Indels DB 21; 100.0%; Score 1237; DB 21 100.0%; Pred. No. 4.3e-62; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 238; Conservative

238 AA;

Sequence

; 0

61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120 9 g δ à

1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASOSVDYDGDSYMNWY

121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 61 q á g

181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 ò

AAW90930 standard; Protein; 238 AA. AAW90930; AAW90930 

08-AUG-2000 (first entry)

Humanised anti-Fas designed light chain Leu 1 protein.

anti-allergic, anti-arthritic; antiviral; immunomodulatory; cardiant; defamatological; immunosuppressive; thyronimhetic; antirheumatic; antirheumatic; antirheumatic; antirheumatic; antirheumatic; antirhertility; neuroprotective; antiarteriosclerotic; hepatotropic; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

EP990663-A2 Synthetic.

05-APR-2000.

99EP-0307711. 29-SEP-1999; 98JP-0276881. 98JP-0276882. 30-SEP-1998; 30-SEP-1998;

(SANY ) SANKYO CO LID.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI; 2000-258930/23. N-PSDB; AAA11631 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 3; Page 156-157; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

complexis in cells with a normal system, by binding to Fas on the cell surface, and prevents

apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antirheumatic, nephrotropic, antilnfertility, neuroprotective,

contiarterioscleroric, cardiant and hepatropic activity. (I) induce

antirheumatic, nephrotropic, antilnfertility, neuroprotective,

contiarterioscleroric, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

complexis by binding to cell surface Fas or inhibit it by competitive

converses associated with the Fas/Fas ligand system, especially systemic

complexishmentosus, Hashimoto disease, remustoid arthritis, graft

versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

consmita, Addison's disease, thrombopenia purpura, insulin

consmita, Addison's disease, thrombopenia purpura, insulin

constitute apoptosis, and antility, allergy, arteriosclerosis, myocardits,

cardiomyopathy, glomerulonephritis, hepatility (fulminat, chronic, viral

contine apoptosis in normal cells but selectively induce it in abnormal

colls. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

the native ligand, do not induce liver disease, and have reduced risk of

the native ligand, antilody light chain construct designated Leu inducing a human anti-murine antibody response. This sequence represents

a humanised anti-Fas antibody light chain construct designated Leu invention. 

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Gaps ; Length 238; Indels Score 1236; DB 21; Pred. No. 4.9e-62; 1; Mismatches 0; 99.68; Query Match
Best Local Similarity 99.69
Matches 237; Conservative

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1 METDTILLWYLLLWYPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple scleroderms; crohn's disease; sterility; myasthenia gravis; multiple sclerodsis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosmodulatory, dermatological, immunosuppressive, thyromimetic, antintremantic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerctic, cardiant and hepatropic activity, (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                              QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised anti-Fas designed light chain Leu 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW90931 standard; Protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANY ) SANKYO CO LTD.
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diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematcosus, Hashimoto disease, rheumatcold arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic luque erythematosus; garft versus host disease; Sjogren syndrome; perintcious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1232; DB 21; Length 238; Pred. No. 8.1e-62;
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glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
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21..238
/label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW83034 standard; Protein; 238 AA.
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/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
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chain of murine anti-human Fas monoclonal antibody HEE7A.

Humanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49F, H80S, P81R, V82L, B84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coll pHSHHS SANK 70398 harbors plasmid pHSHHS carrying a fusion of fragment of the humanised PDHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAM83031-37), like native HFE7A, are capabble of inducing apoptosis in abnormal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thromobenia burpura and insulin-dependent disbetes), allergies, attopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the PDHH type humanised light
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Tohru T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Page 218; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Hideyuki H, Hiroko Y, J
O, Nobufusa S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS
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/label- CDR_L2
/note- "claim 9"
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/label= CDR_L1
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                                                                                                                                                                                                                                                                                                                                                                               (SANY ) SANKYO CO LTD.
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01-APR-1997;
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94.9%; Score 1174; DB 19; Length 238; 93.3%; Pred. No. 1.4e-58;
                               Indels
             Pred. No. 1.4e-58;
9; Mismatches 7;
             Local Similarity ...
 Query Match
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Matches
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy. glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody \,
                                  121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                      1 metdtillwvlllwvpgstgeivltgspgtlslspgeratlsckasgsvdydgdsymnwy
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                                                                                                                                                                                                                                                                                                                AAB14777 standard; Protein; 238 AA.
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                       QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                      TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                          1 METDIILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
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                                   Indels
Pred. No. 1.4e-58;
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                                                                                                                                                                                                                                                                                                                                                                                            AAW90927 standard; Protein; 238 AA.
                                9;
              93.3%;
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98JP-0276882.
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                 Similarity 93.3
2; Conservative
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosalerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus errythematosus, Hashimotto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, starility, myasthenia gravis,
antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1174; DB 21; Length 238;
Pred. No. 1.4e-58;
9; Mismatches 7; Indels 0
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93.3%;
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metdtillwvlllwvpgstgdivltqspgtlslspgeratlsckasqsvdydgdsymnwy METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY

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181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

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This is the amino acid sequence of the HH type humanised light chain of murine anti-human Fas monoclonal antibody HFB7A. Humanisation of the murine sequence (see AAM8304) entailed making P47A, K49R, H80S, PBR, W82L, E84A. E85A, B87F and T89V amino acid substitutions; these residues are conserved in the human light chain (separate) and passent and the human light harbors plasmid pHSGHHY carrying a fusion fragment of the humanised HH type HFB7A light chain and DAN encoding the region of human immunoglobulin Rappa chain, and is deposited as PERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFB7A (see AAW83031-37), like native HFB7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such liseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, green, sieger and syndrome, pernicious anaemia, Addison's disease, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
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Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 199-199; 292pp; English.
21..238
/label= Mat_protein
                                                   /label- Variable
                                                               132..238
/label- Constant
                                                                                                                                    'note= "claim 9"
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/label= CDR_L2
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/label= CDR_L3
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/label= CDR_L1
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                                                                                                                                                                                                                                                                                                                                                                                     97JP-0082953
97JP-0169088
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                                                                                                                                                                                                                                                                                                                                       30-MAR-1998;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, attended and properties, myocarditis, cardiomyopathy, glomerulonephintis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and ABB14777-B14778
                                                                                                                                                                                      murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                    Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                               Humanised anti-Fas antibody light chain, SEQ ID NO:50.
                                                                                                                                                                                                                                                              hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 78-79; 139pp; Japanese.
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                   AAB14772 standard; Protein; 238
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                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                     Chimeric - Mus musculus. Chimeric - Homo sapiens.
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                                                        AAB14772;
AAB14772
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238 AA;

Sequence

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Gaps

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Score 1169; DB 19; Length 238; Pred. No. 2.7e-58; 9; Mismatches 8; Indels 0;

6;

Conservative

Best Local Similarity Matches 221; Conserv

Query Match

94.5%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatorv or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                             QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                   Gaps
                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                         GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                          antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-Fas antibody HFE7A light chain HH type protein.
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 Length 238;
                                 Indels
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   DB 21;
Score 1169; DB 21
Pred. No. 2.7e-58;
9; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                      AAW90922 standard; Protein; 238 AA
94.5%;
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                                221; Conservative
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               Similarity
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                  Best Local
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cc Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic complexes a specially systemic system-actives anemia, Addison's disease, rheumatoid arthitis; graft or anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, anemia, Addison's disease, thrombopenia purpura, insulin dependent diabletes mellitus, allerry, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic mutrhe disease models. (I) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody response. This sequence represents the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; soloroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%; Score 1169; DB 21; Length 238; 92.9%; Pred. No. 2.7e-58; ive 9; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
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Homo sapiens. Synthetic.

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This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coll pHSGHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion fragment of the humanised HM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells. Captressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune classase, graft versus host disease, Sjoren syndrome, pernicious anemia, Addison's disease, Sloren syndrome, pernicious anemia, sterility, mvarthoria ransis multiple solences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thromboenia burpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jun O, Kimihisa I;
, Tohru I;
Location/Qualifiers
                               /label= Sig_peptide
                                           21..238
/label= Mat_protein
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/label= CDR_L2
/note= "claim 9"
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/label= Variable
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Masahiko O, Nobufusa S, Shin Y
                                                                                                                                                                          'note= "claim 9"
                                                                                                                                                                                                                                                      /label= CDR_L3
/note= "claim 9"
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/label= CDR_L1
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25-JUN-1997;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                      61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                            121 TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                              1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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Length 238;
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                                           Indels
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 93.5%; Score 1156; DB 19; 92.0%; Pred. No. 1.4e-57;
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                                         10; Mismatches
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                                       Matches 219; Conservative
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Chimeric - Homo sapiens.
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                       Best Local Similarity
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anti-allergic, anti-arthritic, antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hephrotropic; antininetrility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabates mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                   QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOSNEDPR 120
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                                                                                                                                                                                                                                                                                                                             238
                                                                                                                                                                                                                                                                                                                                         antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory or autoimmune disease, induces apoptosis selectively
cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                             GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody HFE7A light chain HM type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tamaki I, Takahashi T;
                                                                          Length 238;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example reference 14; Page 117-118; 263pp; English.
                                                                                         Pred. No. 1.4e-57; ; Mismatches 9;
                                                                          93.5%; Score 1156;
92.0%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW90923 standard; Protein; 238
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98JP-0276882.
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                                                                                           Best Local Similarity 92.0
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANY ) SANKYO CO LID.
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                                                                                         Similarity
                              238 AA;
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30-SEP-1998;
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 antibodies.
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                              Sequence
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          12
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disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent disbetes mellitus, allery, arterioselscosis, myosarditis, cardiomyopathy, glomerulonephitis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-nurine antibody response. This sequence represents a humanised anti-Fas antibody HEFAA light chain HM type which is used in the method described in the invention.
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                 immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myasthenia grantis, multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; acppy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1156; DB 21
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92.0%;
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us-09-499-662-131.rag

238 AA;

Sequence

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used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                           New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                               Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                              Claim 21; Page 220-221; 292pp; English.
                                   /label= Sig_peptide
21..238
/label= Mat_protein
                      Location/Qualifiers
                                                         21..131
/label= Variable
                                                                               /label= Constant
                                                                                                    'note= "claim 9"
                                                                                                                         /note= "claim 9"
                                                                                                                                       /label= CDR_L3
/note= "claim 9"
                                                                                                          74..80
/label= CDR_L2
                                                                                      44..58
/label= CDR_L1
                                                                                                                                                                                                     97JP-0276064.
97JP-0082953.
97JP-0169088.
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                                                                        32..238
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                                                                                                                                                                                                                                                                             N-PSDB; AAV70078
Homo sapiens.
Synthetic.
                                                                                                                                                                                         30-MAR-1998;
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                                                                                                                                                                                                             01-APR-1997;
25-JUN-1997;
                                                                                                                                                            AU9859701-A
                                                                                                                                                                           08-0CT-1998
                            Peptide
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                                                         Region
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                      Key
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chain of murine anti-human Pass monoclonal antibody HFEFA.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFEFA light chain and boosited as FERM BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFEFA (see AAW83031-37), like native HFEFA, are capable of inducting Apoptosis in abnormal cells. Cells. The humanised antibodies are used to evaluate, in animal cells. The humanised antibodies are used to evaluate, in animal cells. The humanised antibodies are used to evaluate, in animal cells. The humanised antibodies are used to evaluate, in animal cells. The humanised set involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, craft versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arrahist, autoimmune haemolytic anaemia, sterility. Myasthenia gravit militins autoimmune haemolytic anaemia. sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed). This is the amino acid sequence of the PDHM type humanised light

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                     61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                   121 TFGOGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                        Gaps
                                                                                                                                        1 METDTILLEWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                            181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                    ;
Length 238;
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                                                                        Indels
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   DB 19;
                                                         . 6
93.4%; Score 1155; DB 1992.0%; Pred. No. 1.6e-57
                                                                    10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14778 standard; Protein; 238 AA.
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Chimeric - Homo sapiens.
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Query Match
Best Local Similarity
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                                                                    Matches 219;
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glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                          QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                    TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                   Gaps
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                                                                                                                                                                              1 METDTILLMVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                    Length 238;
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                                                                                                                                                   Indels
                                                                                                                      DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised HFE7A designed light chain protein #2.
                                                                                                                   93.4%; Score 1155; DB 2.92.0%; Pred. No. 1.6e-57
                                                                                                                                                  10; Mismatches
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This invention describes a nover numerized anti-ras antibouy-tiake molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ignand system, by bindibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit in by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's Syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, Cor D) or alcoholic), and transplant rejection. (I) selectively induce it in abormal cells but selectively induce it in abormal cells the but selectively induce it in abormal cells unine antiamine active site of Fas, ie. they minic the native ligand, do not induce liyer disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-marine antibody response. This sequence represents the method in the inventione of light chain which is used in the chairs.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-887-352B-15

US-08-887-352B-15

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US-08-887-352B-15

US-09-109-207C-17

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Maximum Match 100%
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Sequence 2, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Pred. No. 5.3e-88;
                                   US-08-437-642B-40

US-09-097-309-2

US-09-097-309-6

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US-09-097-309-6

US-09-097-309-62

US-09-027-449-51

US-09-026-985-62

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

US-09-026-985-51

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US-09-026-985-72

US-09-026-985-72
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION UNDHARE: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
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REGISTRATION UNDRER: 30,946
REFERENCE/DOCKET UNDRER: BOER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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LENGTH:
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121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Sequence No. 5994511
GENERAL INNOFAMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                   Gaps
                                  21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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   2; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-U1-1997
CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTA19 G. RECISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
TELECOMMUNICATION INFORMATION:
TELECHONE: 650/252-1489
TELECHONE: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 mmino acids
TYPE: Amino Acid
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Pred. No. 8.3e-87;
3; Mismatches 3;
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 Mismatches
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Best Local Similarity 97.2%;
Matches 212; Conservative
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COMPUTER READABLE FORM:
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Matches
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88.8%; Score 1099; DB 3; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3: TnAele
181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    Sequence 9, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P0718P2C1D1
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APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRICATION:
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PRICATION NUMBER:
PILING DATE:
PRICATION NUMBER:
PRICATION NUM
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TELECOMMUNICATION INFORMATION:
TELEFAN: 650/252-1489
TELEFAN: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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Amino Acid
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                                                                                                    Length 218;
    ; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: humanized maell, version 1, light chain US-08-466-163B-9
                                                                                                  Score 1099; DB 4; Length 2
Pred. No. 8.3e-87;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/485,819
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/08466163B
; Patent No. 6329509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                  Query Match 88.8%;
Best Local Similarity 97.2%;
Matches 212; Conservative
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SEQ ID NO 9
LENGTH: 218
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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Patent No. 6290957
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT FAPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: us 08/887,352
BARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
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GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.8%; Score 1099; DB 4; Length 218; Best Local Similarity 97.2%; Pred. No. 8.3e-87; Matches 212; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-13
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TYPE: PRT
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SEQ ID NO 1

FEATURE:

Matches

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Sequence 15, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                         81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                             61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
                                                                                                                                            81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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1 DIQLTQSPSSLSASVGDRVTITCRASKPVDGEGDSYMNWYQQKPGKAPKLLIYAASYLES 60
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Pred. No. 1.4e-84;
6; Mismatches 5;
                                                                                                                                                                                                 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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03-Jul-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTAIG G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PILTELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.7%;
Best Local Similarity 95.0%;
Matches 207; Conservative (
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Amino Acid
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APPLICATION NUMBER: US,
FILING DATE: 03-Jul-199
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OPERATING SYSTEM:
SOFTWARE: WinPati
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Pred. No. 7.7e-85;
5; Mismatches 5; Indels
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87.0%; Score 1076; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 7.7e-85;
Matches 208; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1-218
. OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: E27 anti-IgE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
  181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                          Sequence 1, Application US/09282505A
Patent No. 6194551
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: Pl266R1
CURRENT APPLICATION UNDBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ESONE EXINAGUESE IGUSOGIE et al.
TITLE OF INVENTION: POLYPEPLIGE VARIANTS
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09054255 Patent No. 6242195
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 87.0%;
Local Similarity 95.4%;
hes 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Artificial
                                                           RESULT 7
US-09-282-505-1
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US-09-054-255-1
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Gaps

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FEATURE:

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 24, Application US/08887352B; Patent No. 5994511 GENERAL INPORMATION: GENERAL APPLICANT: Henry B. Lowman, Leonan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTA19 G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPASX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%;
95.0%;
                                  : 1 DNA Way
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.7
Best Local Similarity 95.0
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
      CORRESPONDENCE ADDRESS
                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
                          ADDRESSEE:
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                                                                                                          COUNTRY:
                                                                                    STATE:
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                                                                                               Sequence 17, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAR Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Improved Anti-IgE Antibodies and Method of
Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/87,352B FILING DATE: 03-701-1997 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Svoboda, Craig G. REGISTREATION NUMBER: 91123 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1073; DB 2;
Pred. No. 1.4e-84;
6; Mismatches 5;
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GENERAL INFORMATION: APPLICANT: Henry B. Lowman, Leonar TITLE OF INVENTION: Improved Anti-TITLE OF INVENTION: Improving Poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
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95.0%;
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Best Local Similarity
Matches 207; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
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                                                              RESULT 10
US-08-887-352B-17
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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Pred. No. 1.4e-84;
6; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
TITLE OF INVENTION: Inproved Anti-IgE Antibodies and Method of Improving Polypept
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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Patent No. 617213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypep
FILE REFERENCE: P1123R1
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
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               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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86.7%; Score 1073; DB 4;
Best Local Similarity 95.0%; Pred. No. 1.4e-84;
Matches 207; Conservative 6; Mismatches 5;
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SEQ ID NO 19
LENGTH: 218
TYPE: PRT
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NAME/KEY: Artificial
LOCATION: 1-218
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US-09-109-207C-17
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1073; DB 2; Length 2:
Pred. No. 1.4e-84;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-15
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95.0%; Pred. No. 1.4e-84;
live 6; Mismatches 5;
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03-Jul-1997
11: 530
        CURRENT APPLICALL...
APPLICATION NUMBER: US/08/88/,2222
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CTRAIG G
REGISTRATION NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPAN: 650/225-1489
TELEFAN: 650/225-1489
TELEFAN: 650/225-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: Amino Acid
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%;
95.0%;
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Best Local Similarity 95.0°
Matches 207; Conservative
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US-08-887-3528-24
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Best Local Similarity
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) ORGANISM: Artificial
FEATURE:
) NAME/RET: Artificial
LOCATION: 1-218
) OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
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                                                                                      Length 218;
                                                                                       Query Match 86.7%; Score 1073; DB 4; Length 2 Best Local Similarity 95.0%; Pred. No. 1.4e-84; Matches 207; Conservative 6; Mismatches 5; Indels
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Scoring table:

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717 715.5 705.5 705.5 702.5 696 692.6 686.5 675.5 607.5 608.5 607.5 607.5 608.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.5 607.

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Gaps

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215;

Length Indels

5,

homology

57

177

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C; Accession: JE0241
R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998
A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JE0241
A; Reference number: JE0241
A; Accession: JE0241
A; Accession: JE0241
A; Accession: JE0241
A; Residues: 1-216 < ALI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
E; 16-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 IFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLS 178
                                                                                                                                                                                                                                                                                                                                      58 GIPDRESGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEIKRTVAAPSVF
                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ-PKLLIW-ANVRES
                                                                                                                                                                                                                                                             GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF
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                                                                                                                                                                                                                                       21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                    81 GIPSRESGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF
                                                                                                                                                                                                                                                                                                                                                                                               IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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                    A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.8%; Score 876; DB 2; Best Local Similarity 79.4%; Pred. No. 3.3e-50; Matches 173; Conservative 16; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                          71.7%; Score 886.5; DB 2 ilarity 82.0%; Pred. No. 6.9e-51; Conservative 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 STLTLSKADYEKHKVYAGEVTHOGLSSPVTKSFNRGE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
                                                                                                                                                            Query Match
Best Local Similarity
Matches 178; Conserv
    A; Status: preliminary
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C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Fitler: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl A;Reference number: A23746; MUID:91131575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.; Yamaki, S.; Kazi, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: A new subgroup of k type light chains (VkV) identified in cases of A; Reference number: {\tt JE0243}
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C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                          GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNE-DPRTFGQGTKVEIKRTVAAPSV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK-RTVAAPSV 139
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                                                                                                                                        80
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                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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                                                          Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-215 <ALT:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.; Yamagata,
                                                                   ,5e-53;
-,18;
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                                                                                                                                                                                                                                                                                                                                                                                           238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.0%; Score 902.5; DB 2
81.3%; Pred. No. 6.3e-52;
                                                          В
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83.6%; Pred. No. 1...
''n 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda,
submitted to JIPID, November 1998
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor - human
                                                      Query Match
Best Local Similarity 83.6'
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 81,3
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain NIG93
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                                                                                                                                                                                                                                                                                                                                                                                                              177
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Indels

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Length 216;

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If Xappa chain V region (Mabl3-1) - mouse (fragment)
NyAlternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68241; S68244
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, submitted to the BMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porpha, A;Reference number: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphy-A; Reference number: $68211; MUID: 96085223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Modecule type: mRNA
A,Residues: 1-218 <TAK>
A,Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
A,Cross-references: EMBL:D29670; NI: Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka
K;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, Chain-porphy.
FEBS Lett. 375, 273-276, 1995
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: 3316
A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: 533161
A;Accession: S33161
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIPSRFSGSGSGTDFTLT1SSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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Pred. No. 6.9e-42;
y, Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; which is a nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 'NI',3-212 <TAM> A; Residues: 'NI',1-25670 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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63.8%;
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A; Residues: 1-230 <FOL>
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Best Local Similarity
Matches 139; Conserv
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                     R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7922, 1989

A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA A;Reference number: S06084 MUD: 90016888

A;Recession: S06084

A;Mccession: S06084

A;Mcsiques: 1-240 CKRO>
A;Residues: 1-240 CKRO>
A;Cross-references: EMBL:X16129; NID: 956457; PIDN: CAA34256.1; PID: 956458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer: immunoglobulin
C;Reywords: heterotetramer: standard sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-240/Product: 1g kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igrappa chain precursor (15C5) - mouse (5 papea chain precursor (15C5) - mouse (5 papea) with musculus (house mouse) (5 pate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 (5 pate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 (5 pate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 (7 pate: 27 pat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 METDIILLMVLLLMVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGD--SYMN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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Pred. No. 2.6e-42;
5; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 808; DB 2; Length 24 64.2%; Pred. No. 9.7e-46; Live 32; Mismatches 52; Indels
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60.1%;
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Best Local Similarity 60.19
Matches 143; Conservative
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Best Local Similarity 64.2°
Matches 154, Conservative
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A, Cross-references: EMBL: C, Superfamily: immunoglob C, Keywords: heteroterame F; 36-110/Domain: immunoql
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R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr A;Reference number: JC5810; MUID:98063277
A;Accession: JC5810
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19 kappa chain precursor - mouse
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Accession: 501320
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
But. J. Blochem: 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A; Reference number: 501320; MuID:88329081
A; Accession: 501320
A; Molecule type: mRNA
A; Residues: 1-234 CDE1>
A; Molecule type: mRNA
A; Residues: 1-234 CDE1>
A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
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                   Gaps
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                                                                DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                              7 LLWVLLLW-VPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPG
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                                                                                                                                                                                                                                          SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                         monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: This catalytic antibody has peroxidase oxidase. It is C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-94/Domain: immunoglobulin homology <IMM>
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels
. 7.9e-42;
cches 47;
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64.2%; Pred. No. 9.3e-42;
ive 30; Mismatches 48
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                  Mismatches
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61.8%;
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                144; Conservative
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Best Local Similarity
Matches 144; Conser
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Best Local Si
Matches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-234/Product: Ig Kappa chain #status predicted <MAT>F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234;
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llarity 57.9%; Pred. No. 1.5e-40;
Conservative 38; Mismatches 55;
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Matches 135; Conservative
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       C; Accession: A56169
R; Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
J; Biol. Chem. 270, 6628-6638, 1995
A; Title: Recombinant antibodies in bioactive peptide design.
A; Reference number: A56169; MUID:95204454
A; Reference number: A56169; MUID:95204454
A; Reference number: Decliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-210 < MON>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C:Decises: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
B:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Accession: S37484
A:Accession: S37484
A:Accession: S37484
A:Accession: S37484
A:Accession: T-225 CDUC>
A:Accession: T-225 CDUC>
A:Boloule type: mRNA
A:Residues: T-225 CDUC>
A:Accession: T-225 CDUC>
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
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61.4%; Pred. No. 9.2e-40;
tive 30; Mismatches 53;
                                                                                                                                                                                                                                                             58.0%; Score 717; DB 2; 64.6%; Pred. No. 6.9e-40; ive 29; Mismatches 45;
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STLTLTKDEYERHNSYTCEATHKTSTSPI 209
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C;Species: Mus musculus (house mo
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Best Local Similarity
Matches 135; Conserv
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A; Title: Cloning and characterization of cDNAs coding for heavy and light chains of a A; Reference number: PC4202; MUID:97082978
A; Reference number: PC4202; MUID:97082978
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-219 KKWA
A; Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-dems1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>
                                                                                                                                 Y.B.; Han, M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                            C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
AsKwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han,
Gene 173, 257-259, 1996
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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
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August 14, 2002, 15:23:13; Search time 53.64 Seconds (without alignments) 171.798 Million cell updates/sec
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1237
1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descripti	P01834 homo
SUMMARIES		HUMAN
O)	ID	KAC
	DB	1 KA
	Length	106
ď	Query Match	44.3
	Result Query No. Score Match Length DB	1 548 44.3 106 1 KAC HUMAN
	Result No.	-

	Description	P01834 homo sapien	P01661 mus musculu	P01658 mus musculu	P01665 mus musculu	P01666 mus musculu	mus m	homo	homo	mus m	mus n	homo	mus n	homo	homo	homo	homo	P06314 homo sapien	homo	homo	homo	рошо	homo	homo	рошо	mus m	homo	homo	homo	homo	homo	homo	1 homo	P04432 homo sapien
SUMMARIES	ć.	KAC_HUMAN P		KV3F_MOUSE P	KV3M_MOUSE P																												_	KV1X_HUMAN P
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ď	Query	44.3		42.0	39.1	39.0	38.8	38.8	38.7	38.6	37.9	37.2	37.1	37.0	36.5	36.2	36.1	36.1	36.0	35.9	35.9	35.9	35.7	35.6	32.6	35.3	35.1	35.0	35.0	4	4	4	34.6	34.6
	Score	548	531	520	484	482	480	479.5	479	477	469	460	459.5	457.5	451	448	447	447	445	444	444	444	441	440	440	437	434	433	432.5	431.5	429	428	428	428
	Result	1	7	e	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P01662 mus m P06311 homo P06311 homo P011663 mus m P011612 homo P011670 mus m P011596 homo P01596 homo P01433 homo P06413 homo P06510 homo P06510 homo P06510 homo P06510 homo P01659 mus m		ata; Euteleostoridae; Homo. Edelman G.M.;	noglobulin. X.	unn N.; ture of a monoclonal 3 (Bence-Jones protein its significance for	'. Jr., Leder P.; onstant and J region ";	, Langer B., Ponstingl H., e S.; On, pp.57-74, Academic Press, Bence Jones protein Cum (Kappa
34	MAN 018 018 11-4 6-0					RN 191 RA SEQUENCE (BENCE-JONES PROTEIN ROY). RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., RA Steinmetz-Kayne M., Suter L., Watanabe S.; RL (In) Franck F., Shugar D. (eds.); RL Gamma globulins: structure and function, pp.57-74, Academic Press. RL New York (1969). RN 161 RN SEQUENCE (BENCE-JONES PROTEIN CUM). RN MEDLINE-68242259; PubMed-5586923; RA Hilschmann N.; RT "The complete amino acid sequence of Bence Jones protein Cum (kapp. RT Type).";

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121 TFGQGTKVEIK 131
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Best Local Similarity
Matches 98; Conserv
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P01658;
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SEQUENCE
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                       Science 169:56-59(1970).
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
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Wakaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                              Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3550(1969).
                                                                                                                       MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FIId=VAR_003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

W; 51984DIFDD372CE8 CRC64;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region MOPC 63 precursor.
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                                                                                                           SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
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                         SEQUENCE (BENCE-JONES PROTEIN AG)
                                     MEDLINE-69234734; PubMed-4893682
                                                                                                                                                                                                             MARKER, 45-ALA AND 83-LEU.
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InterPro; IPR003597; Ig_cl.
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PROSITE; PS00290; IG_MHC; 1.
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106
83
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P01661;
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MEDLINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                             SEQUENCE OF 21-131.
MEDLINE=73140225; PubMed=4691517;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-III REGION MOPC 63.
                                                Burstein Y., Schechter I.; "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSM6.
PRSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
Differ Co. IPR003596; Ig_V.
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ilarity 74.8%; Pred. No. 5.7e-36;
Conservative 19; Mismatches 14;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE=78235887; PubMed=98179;
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21 DIVLIQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
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FRAMEWORK-2.
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Pred. No. 2.7e-32;
9; Mismatches 11; Indels
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 yappa chain V-III region PC 7183.
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Nature 276:785-790(1978).
PIR; BO1937; KVMS83.
HSSP; PO1789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
FRan; PF00047; Ig; 1.
SMART; SM00406; IGv.
Immunoglobulin V region.
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HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                      Nature 276:785-790(1978)
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Best Local Similarity
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ID KV3N_MOUSE
AC P01666;
DT 21-TT
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-!- MISCELLANGOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
BENCE-JONES PROPEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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MEDILNE=7314024; PubMed=4120629;
MECRAIN D. J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                  Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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COMPLEMENTARITY - DETERMINING - 3.
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KV3M_MOUSE

ID KV3M_MOUSE
STANDARD; PRT; 111 AA.
AC PO1665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 12-JUL-1986 (Rel. 01, Last sequence update)
DT 12-JUL-1998 (Rel. 38, Last sequence update)
DT 12-JUL-1999 (
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               SEQUENCE OF 1-37.
MEDLINE=78235887; Pubmed=98179;
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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121 TFGSGTKLEIKR 132
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132 AA;
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                                                                                                                   1 DIVLIQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                               21 DIVLTQSPSSLSASVGDRVT_ITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                Length 111;
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Pred. No. 5.5e-32;
9; Mismatches 12; Indels
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                                                       11; Indels
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                Score 482; DB 1;
Pred. No. 3.8e-32;
                                                                                                                                                                                                                                                                                                                  KV30_MOUSE STANDARD; PRT; 111 AA. P01667; 21-JUL-1986 (Rel. 01, Created) 21-JUB (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-III region PC 6308.
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                                                       10; Mismatches
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12071 MW;
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PIR; C01937; KVMSOB.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
Immunoq1obulin V region.
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                39.0%;
81.1%;
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Local Similarity 81.1%;
hes 90; Conservative
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ID KV3L_HU
AC P18135,
DT 01-NOV-
DT 15-JUL-
DE 19 kapp
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61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
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MEDLINE-85014148; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the Kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somat:
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167: 840-852(1988).
-!- DISEASE: THE PROPEN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBOTES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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JK1 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73-406-1987 (Rel. 05, Created)
13-A06-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region Walker precursor.
Homo sapiens (Human).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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14073 MW;
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HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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sapiens (Human).
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129 AA;
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                                                                       NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                       IG KAPPA CHAIN V-I REGION WALKER.
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COMPLEMENTARITY - DETERMINING - 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 7769.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA.
                                                                                                                                                                                                                                                      SIMILARITY.
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                                                                            EMBL; X00965; CAA25477.1; ALT_TERM. PIR; A01883; KIHUWK.
HSSP; PO1607; IREI.
INTERPRO; IPR003006; Ig_MHC.
INTERPC; IPR003596; Ig_V.
Pfam; PF00047; Ig'. 1.
SWART; SM00406; IGV: 1.
Immunoglobulin V region; Signal.
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PIR; E01937; KWMS69.
HSSP; P01789; IMCP.
INTERPO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffan; FF00047; Ig'. I.
SMART; SM00406; IGv; I.
Immunoglobulin V region.
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MCKean D.J., Bell M., Potter M.;

McKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WYELOWA PROTEIN. PIR; A01936; KWSC1.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_W.

Pfam; PF000047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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; Pred. No. 9.6e-32;
11; Mismatches 11; Indels
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                 COMPLEMENTARITY-DETERMINING-1.
                                                     COMPLEMENTARITY - DETERMINING - 2.
                                                                                           COMPLEMENTARITY - DETERMINING - 3
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                                                                                                                                                                   6FAA345279356829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 111 AA
                                                                                                                               BY SIMILARITY.
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                                     FRAMEWORK - 2
                                                                                                             FRAMEWORK - 4
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NCBI_TaxID=9606;
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P18136;
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KV3M_HUMAN
   RRAKET AND CONTRACT OF A LANGE OF
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                                                                                                                                                                                                                                                                                MEDLINE-71032830; PubMed-4097974; Watanabe S., Hilschmann N.; Watenabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                      Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 460; DB 1; Length 108; 79.5%; Pred. No. 2.1e-30; Live 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7210.
                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin V region; Bence-Jones protein.
                                                                                           108 AA
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BY SIMILARITY.
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SEQUENCE.
MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11671 MW;
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                                                                                           STANDARD;
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P01600;
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P01668;
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Best Local S:
Matches 899
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88171307; PubMed-3127527;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

T. Exp. Med. 167:840-852(1988).

-I. DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 3.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING - 2. FRAMEWORK - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                  69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     37.1%; Score 459.5; DB 1;
79.3%; Pred. No. 2.4e-30;
Live 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.1007-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region HIC precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA
                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                  11950 MW;
                                                 Nature 276:785-790(1978).
PIR; D01937; KVMS10.
HSSP; P01789; 1MC.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 79.39
Matches 88, Conservative
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                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                             61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-75059122; PubMed-4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Laure Primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).

-i. MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-i. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                          1 METDTILLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                    4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hómo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             3,
                                                                                                                                                                    Query Match
37.0%; Score 457.5; DB 1; Length 129;
Best Local Similarity 68.2%; Pred. No. 4.2e-30;
Matches 90; Conservative 16; Mismatches 23; Indels 3
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
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                                                                                                MW; 7395528EA2BB74D6 CRC64;
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Pred. No. 1.1e-29;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region GAL.
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BY SIMILARITY.
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78.6%;
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PIR: A01867; KIHGGL.
HSSP, P01607; 1REL
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Best Local Similarity 78.6
Matches 88; Conservative
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129 AA;
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P01599;
                    DOMAIN
DISULFID
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SEQUENCE
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DOMAIN
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**REDLINE=77038198; PubMed=824717;

**REDLINE=77038198; PubMed=824717;

**REDLINE=77038198; PubMed=824717;

**Capra J.D., Klapper D.G.; Red P.G.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-2.
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38, Last annotation update)
                                                                                                                                                   108 AA
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Ig kappa chain V-I region Lay.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

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Q99m37 mus musculu Q91wf8 mus musculu Q91w59 mus musculu Q97la5 mus musculu Q91w12 mus musculu Q91x10 homo sapien Q94l81 homo sapien Q94l81 homo sapien Q94l79 homo sapien Q94l79 homo sapien Q95pff homo sapien Q92pff homo sapien Q95pff homo sapien Q95pff homo sapien Q95pff homo sapien Q9178 homo sapien
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SUMMARIES
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Q91WF8
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Q91W12
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Q920E9
Q9UL78
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                                 11111144
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Match Length
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Gaps

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60.3%; Score 745.5; DB 11; Length 238; 58.1%; Pred. No. 9.1e-58; Indels 1; ive 41; Mismatches 56; Indels 1;

Best Local Similarity 58.1 Matches 136; Conservative

Query Match

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*

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SEQUENCE FROM N.A.
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                                         65 GKAPKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                      65 GQSPKLLIXKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGS 124
                                                                                    125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              091WS9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mus musculus (Mouse).

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                        181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                              185 ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 234;
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                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2001) to the EMBL/GenBank/DDBJ database EMBL; BC015292; AAH15292.1; -- Hypothetical protein. SEQUENCE 234 AA; 25929 MW; BOD0B0E6EB7812D2 CRC64;
                                                                                                                                                                                                                 091MFB;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%; Score 738; DB 11;
59.7%; Pred. No. 4.1e-57;
ive 34; Mismatches 58;
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Best Local Similarity 59.78
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, is 11ght and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAP-1199) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS2371; AAD40242.1;
HSSP; P01679; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 LIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEI 130
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                         Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 233
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                                                       the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           233 AA; 25781 MW; B1C184DA149A16EB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                       59.6%; Score 737; DB 11;
62.7%; Pred. No. 4.9e-57;
iive 29; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.5%; Score 724; DB 11;
62.8%; Pred. No. 6.1e-56;
ive 31; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00290; IG_MHC; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
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TISSUE-COLON;
Strausberg R.;
Submitted (SEP-2001) to the
EMBL; BC013496; AAH13496.1;
                                                                                                                                                                                                                                                                     Best Local Similarity 62.78
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 62.8%
Matches 137; Conservative
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                                                                                                       Hypothetical protein.
NON_TER 1
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214 AA;
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SECUENCE
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Q9UL77
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200
                                                                                      LESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A., Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                              IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.0%; Score 704.5; DB 11; Length
60.6%; Pred. No. 3.6e-54;
Live 32; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006643; AAH06643.1; -. SEC73BDEBD5E8FEF CRC64; SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                                                                                                                                                                          Q91W12 PRELIMINARY; PRT; 235 AA. Q91W12; U-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) UNKNOWN (PROTEIN FOR MGC:6582).
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                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 60.6
Matches 134; Conservative
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TISSUE=BREAST TUMOR;
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STRAIN-C57BL/6J; TISSUE=KIDNEY;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
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                              Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomuza K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Mayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/64; TISSUE-KIDNEY; MEDLINE-20530913; PubMed=11076861; Shibata K., Ttoh M., Alzawa K., Naqooka S., Sasaki N., Carninci P., Shibata K., Ttoh M., Alzawa K., Naqooka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Coneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rakki Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; EMBL; AK002514; BAB22154.1;
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CONSOrtium.;
"Functional annotation of a full-length mouse cDNA collection.";
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8
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                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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Pred. No. 4.2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
Carificiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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tive 33; Mismatches
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
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80 26

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21 DIVLIQSPSSLSASVGDRVIITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                        81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 36.3%; Score 449; DB 4; Length 108; 1. Similarity 77.7%; Pred. No. 3.8e-32; 87; Conservative 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                            Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REATIVE IMMUNGGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                       81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -. HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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MEDLINE-98277139; PubMed~9614934;
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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Matches 87; Conserv
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108 A
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                                                                                                                                                                                                                                                              (FRAGMENT)
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NON_TER
SEQUENCE
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                                                                                                                                                                          Q9UL70
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Q9UL70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin_reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-STREPTOCOCCAL/ANTI-NYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 462.5; DB 4; Length 107;
Pred. No. 2.4e-33;
7; Mismatches 7; Indels 5,
                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 470; DB 4; Length 108;
Pred. No. 5.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                     108 AA; 11738 MW; CO6681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1;
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                38.0%;
82.1%;
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83.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Conservative
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 PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGV; 1.
                                                                                                 Homo sapiens (Human).
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                         NCBI_TaxID=9606;
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01-DEC-2001
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SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiéns (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
          Myosin-reactive autoantibodies in rheumatic carditis and normaletus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.2%; Score 436; DB 4; Length 108; Best Local Similarity 76.8%; Pred. No. 5.3e-31; Matches 86; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                               107 107 107 107 107 AA; 11501 MW; 070549FDE0754748 CRC64;
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                                                                                                                                                                                                                                                                                           Query Match 35.4%; Score 437.5; DB 4; Best Local Similarity 77.7%; Pred. No. 3.9e-31; Matches 87; Conservative 10; Mismatches 10;
                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGv. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035035; AAD56271.1; -
HSSP; P01607; IREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA
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SMART; SM00406; IGV; 1.
NON_TER 108 108
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                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
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SEQUENCE
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Q9UL79
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81 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21361171; PubMed=11468171; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell blunden."; Blood 98:714-720(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%; Score 432; DB 4; Length 116; 70.0%; Pred. No. 1.3e-30; Live 15; Mismatches 17; Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 116
116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
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                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last anotation update)
KAPPA I LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.4 KDA PROTEIN.
116 AA.
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InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_11ke.
InterPro; IPR003600; Ig_11ke.
InterPro; IPR003600; Ig_NHC.
InterPro; IPR003596; Ig_V.
SMART; SM00409; IG; 2.
SMART; SM00400; IG; 2.
SMART; SM00410; IG_1; 1.
SMART; SM00410; IG_1; 1.
SMART; SM00410; IG_1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
HYDOTHetical protein.
SEQUENCE 235 AA; 25403 MW; 39807BFF
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NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               67 APKLLIYAASNLESGIPSRFSGS - GSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                     125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 APKLLIYAASNLESGIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ--QSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGN 182
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                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLWVLLLWVPGSTGDIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
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Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;
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TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:17259).
   Pred. No. 4.5e-30;
3; Mismatches 86;
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41.9%; Pred. No. 7.4e-30;
Live 40; Mismatches 87;
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                              Matches 100; Conservative
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Best Local Similarity
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Gaps
                                             SEQUENCE FROM N.A. Athings I.G., Horaitis O., Cotton R.G.H.; Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
                                                                                                                                                                                                                                                                                                                 21 DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES 80
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ilarity 71.2%; Pred. No. 4.7e-29;
Conservative 13; Mismatches 19;
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Matches 79; Conserv
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:01:42 ; Search time 230.21 Seconds (Without alignments) 38.599 Million cell updates/sec

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1 SYWMQXXXXXXXXXXXXXXXE....XXXXXXXXXXNRDYSNNWYFDV

Title: Perfect score: Sequence:

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747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti-Fas MAb HFE7A Mouse anti-Fas ant Murine anti-Fas an Anti-Fas humanised Anti-Fas humanised Humanised anti-Fas Humanised anti-Fas Humanised HFE7A de Anti-Fas humanised Humanised anti-Fas Fragment of humani Description SUMMARIES AAW90897 AAW83036 AAW83037 AAB14776 AAB14779 AAW90926 AAW83041 AAB14747 AAW83038 AAB14775 AAW90925 П 2113113113 Length DB Query Match 1 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Score 110 110 110 . 9 Result

Humanised HFE7A de Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas Humanised HFE7A de	Anti-EGFR antibody Anti-EGFR antibody Anti-DNA antibody Anti-DNA antibody	antib BB he antib eader	SCFV(FMFJ): STUC FWP51 fusion prote (FRP51)-ETA fusion Anti-DNA antibody Protein sequence o Murine Act-1 heavy	Consensus protein Heavy chain of a h Murine 66425 heavy Humanised 66425 F( Humanised murine 6	Murine Gotas neavy Humanised 66425 F( Single chain Fv an Anti-up54 Mab T16 Anti-up54 MAb T16 Monoclonal antibod Anti-IL-8 MAB 664. Anti IL-8 antibody Anti IL-8 metabody
21 AAW90929 21 AAW90933 21 AAW90934 21 AAW90935 21 AAW90936	6 AAR79861 6 AAR79863 8 AAW04586 8 AAW04589	AAW0743 AAY9215 AAW0459 AAB7084		AAW5381 AAW5381 AAW5381 0 AAW5945 0 AAY2945 1 AAB3031 1 AAB3031	11 AAY/7754 12 AAB70762 22 AAB70762 23 AAW2680 24 AAW2680 25 AAW4232 26 AAW4232 27 AAW31579
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12 13 14 15	11 118 119 20	22 23 24 24	200 200 300 300 300		33 3 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

AAW83038 standard; Protein; 145 AA AAW83038 RESULT 

AAW83038;

15-MAR-1999 (first entry)

Anti-Fas humanised antibody HFE7A heavy chain variable region.

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pennicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; actoriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

1..19 /label= Sig_peptide 20..145 /label= Mat_protein Socation/Qualifiers Peptide

Region

Protein

50..54 /label= CDR_H1 /note= "claim 9" 69..84

Region

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JP2000169393-A.
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                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the VD type humanised heavy chain variable region of murine anti-human Fas monoclonal antibody HFETA. It was utilised in a claimed humanised HFETA heavy chain (see AAV70079). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA (see AAW83031-37) are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. Humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Slogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's alsease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomecular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all olaimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 sywmqwvkqapgqrlewmgeidpsdsytnynqkfkgkatltvdtsastaymelsslrsed 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; DB 19; Length 145; 1.4e-11;
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                                                                                                                                                                                                                   Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.46
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 246;
                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 207; 292pp; English.
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/label= CDR_H2
/note= "claim 9"
118..129
                                  /label= CDR_H3
/note= "claim 9"
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97JP-0169088.
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                                                                                                                                                                                                                                                       WPI; 1998-543440/47.
N-PSDB; AAV70104.
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Best Local Similarity
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                                                                                                                      30-MAR-1998;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the FaS/FaS ilgand system containing an anti-FaS antibody as the active component. The anti-FaS antibody is either the murine anti-human FaS monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRS (complementarity determining regions) to antibody HFETA. Via its interaction with FaS, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerois, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoinmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody ^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Fragment of humanised anti-Fas antibody heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 246; DB 21;
42.5%; Pred. No. 1.4e-11;
tive 46; Mismatches 0;
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Chimeric - Homo sapiens.
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N-PSDB; AAA72146.
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61 XXXXXXXXNRDYSNNWYFDV 80

DP OY

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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

c apoptosis in cells with a normal system, by inhibiting binding between

apoptosis in cells with a normal system, by inhibiting binding between

c apoptosis in cells with a normal system, by inhibiting binding between

c anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antirheumatic, nephrotropic, antinfertility, neuroprotective,

c limbition of ligand binding. (I) are used to treat and/or prevent

c diseases associated with the Fas/Fas ligand system, especially systemic

c lupus erythematosus, Hashimoto disease, pernicious or hypoplastic

c versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

c anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

c disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

c anemia, Addison's Basedow's disease, thrombopenia purpura, insulin

c dependent diabetes mellitus, allergy, arteriosclerosis, myccarditis,

c ardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

c inhibit apoptosis in normal cells but selectively induce it in abnormal

c inhibit apoptosis in normal cells but selectively enteriors or allergy and transplant rejection. (I) salectively
                       anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; demachological; immunosperssive; thyrominetic; antirhematic; anti-respondentation immunosperssive; thyrominetic; antirhematic; anti-respondent information anti-respondent of seasons; neumanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
  antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example reference 15; Page 126-127; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells with abnormal Fas-Fas ligand systems
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; systemic lupus ernicitus anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region; monoclonal antibody; mouse; Fas; humanised antibody; Hideyuki H, Hiroko Y, Jun O, Kimihisa I; O, Nobufusa S, Shin Y, Tohru T; label- Sig_peptide 0..464 label- Mat_protein 0..140 Location/Qualifiers AAW83041 standard; Protein; 464 AA. 141..464 /label= Constant /note= "claim 9" 'label- Variable 'note- "claim 9" /label= CDR_H3 /note= "claim 9" Anti-Fas MAb HFE7A heavy chain. 50..54 /label= CDR_H1 label = CDR H2 97JP-0082953 98AU-0059701 97JP-0276064 15-MAR-1999 (first entry) .128 (SANY ) SANKYO CO LTD. WPI; 1998-543440/47. N-PSDB; AAV71029 Mus musculus. Masahiko O, 30-MAR-1998; AU9859701-A. 08-OCT-1997; 25-JUN-1997; 01-APR-1997; 08-OCT-1998 AAW83041; Akio S, Peptide Protein HFE7A; Region Region Region Region Region 110 AAW83041 RESULT g A PROPERTIES OF A PROPERTIES O

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EP990663-A2
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                             This is the amino acid of the heavy chain of murine anti-human Fas monoclonal antibody HFE7A. CDNA (see AAV70129) encoding the heavy chain was obtained from HFE7A-secreting hybridoma (FEMA BP-58A8).

RNA by RT-PCR (see AAV70125-26). The invention provides humanised artibodies are capable of inducing apoptosis in abnormal cells. HFE7A antibodies are capable of inducing apoptosis in abnormal cells. expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's diseases (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, solecoderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death;
         Reference Example 4; Page 187-188; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse anti-Fas antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB14747 standard; Protein; 464 AA.
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                                                                                                                                                                                                                                                                                                              Query Match
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                                                              The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arterfosels, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS heavy chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 246; DB 21; Length 464; 42.5%; Pred. No. 3.9e-10; Live 46; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine anti-Fas antibody HFE7A heavy chain protein.
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Example 4; Page 67-68; 139pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW90897 standard; Protein; 464 AA.
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N-PSDB; AAA11546.
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Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 AA;
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Homo sapiens.

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This invention describes a novel humanized anti-Fas antibody-like
molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
capoptosis in cells with a normal system, by inhibiting binding between
cantianemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
cantiartriosclerofic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit in by competition
canenia, Addison's disease, sloracderma, Goodpasture syndrome, Crohn's
clievase, autoinmune hemolytic anemia, sterility, myasthenia gravis,
canemia, Addison's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
culting a human anti-murine antibody response. This sequence represents
a murine disease models. (I) act on the active site of Fas, i.e. they minc
che native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
capacity in a normal cells but segonse. This sequence represents
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                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 246; DB 21; Length 464;
Pred. No. 3.9e-10;
Mismatches 0; Indels 0
                                                                                                                 Example reference 4; Page 100-102; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100.0%; Score 246; C
Local Similarity 42.5%; Pred. No. 3.9e
hes 34; Conservative 46; Mismatches
                                                                   cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW83036 standard; Protein; 470 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA;
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Matches
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chain of murine anti-human Fass monoclonal antibody HFE7A. E. coll pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion of fragment of the humanised vor tregion (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised creations of HFF7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sjögren syndrome, pernicious anaemia, Addison's disease, scleroderma Goodpasture syndrome, Crohn's disease, rhemmatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of the VD type humanised heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
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                                          .ocation/Qualifiers
                                                                      label Sig_peptide
                                                                                  0..470
label Mat_protein
                                                                                                                20..140
/label- Variable
                                                                                                                                                                                                   /note= "claim 9"
69..84
                                                                                                                                            41.464
Tabel Constant
                                                                                                                                                                                                                                  /label = CDR_H2
/note= "claim 9"
118..129
                                                                                                                                                                                                                                                                                /label= CDR_H3
/note= "claim 9"
                                                                                                                                                                            50..54
/label= CDR_H1
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97JP-0169088.
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25-JUN-1997;
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            Synthetic.
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                                                        Peptide
                                                                                      Protein
                                                                                                                   Region
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DB 19; Length 470;

100.0%; Score 246;

Query Match

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JP2000169393-A.
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                                        Gaps
                                                                      SYWMQXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systematic lupus erythematrosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopic sclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AlDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
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Tohru T;
                    4.1e-10;
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                   Pred. No. 4.1
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Masahiko O, Nobufusa S, Shin Y, Tohru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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'label Sig_peptide
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/label= Mat_protein
                                                                                                                                                                                                                                                                        AAW83037 standard; Protein; 470 AA.
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/label= CDR_H3
/note= "claim 9"
42.58; Pic. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20..140
/label= Variable
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/label= CDR_H1
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                                                                                                                                                                 110 tavyycarnrdysnnwyfdv 129
                                                                                                                                            61 XXXXXXXXNRDYSNNWYFDV 80
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97JP-0082953.
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                                    Conservative
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N-PSDB; AAV70080.
               Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the HV type humanised heavy

chain of murine anti-human Fas monoclonal antibody HFE7A. It
includes humanishing R44G and A7GT anino acid substitutions that are
are conserved in the human Egg heavy chain. Host Escherichia coli
geHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion
fragment of the humanised HV type HFB7A heavy chain and DNA
encoding human 1gG1 constant region (see AAV70080), and is deposited
as FERW BP-6273 (claimed). The invention provides methods for
producing humanised antibodies by culturing host cells. Humanised
versions of HFB7A (see AAM83031-37), like native HFB7A, are capable
of inducing apoptosis in abnormal cells. The humanised
inhibiting Fas-induced apoptosis in normal cells. The humanised
antibodies are used to evaluate, in animal models, treatments of
diseases that involve FasyFas ligand interactions, and also to
treat such diseases, including autoimmune disease, scleroderma,
Goodpasture syndrome, pernicious anaemia, Addison's disease, scleroderma,
Goodpasture syndrome, Crohn's disease, thrombopenia purpura and
insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
multiple scl rosis, Bassedow's disease, thrombopenia purpura and
insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
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                                                                                                                                                                                                                       Claim 22; Page 225-227; 292pp; English.
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Chimeric - Homo sapiens
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Best Local Similarity
Matches 34; Conser
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(SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFFTA. Or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFFTA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the areatment or prevention of conditions such as autoimmune diseases, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                            Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                           Claim 21; Page 95-96; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14779 standard; Protein; 470 AA.
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           98JP-0276883.
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Matches 34; Conservative
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                                   (SANY ) SANKYO CO LID.
                                                          WPI; 2000-485645/43.
N-PSDB; AAA72159.
                                                                                                                                                                                                                                                                                                                                                         470 AA;
                                                                                                                      anti-Fas antibody
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           30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                       The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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                                                                                                                                                                                                                                                                   Claim 21; Page 108-109; 139pp; Japanese.
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Matches 34; Conservative
WPI; 2000-485645/43.
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                                       N-PSDB; AAA72184
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98JP-0276881

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hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
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                                                                                                                                                                                                                                                                                                                                           This invention describes a novel numnized anti-ras antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas indecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas indecule (I) that, induces apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antidiabetic, antidiffertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit the by competitive inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent of inhibit expensively system, system, especially systemic lupus expthematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoinmune hemolytic anemia, sterility, mysathenia gravis, anitiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, hepatitis (fulminant, chronic, viral (B), C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic multiple a humanised anti-marine antibody HREAA designed heavy chain which is used in the method described in the invention.
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                                                                                                                                                                                              New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                       Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 470;
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                                                                                                                                                                                                                                                                                      Example reference 15; Page 134-136; 263pp; English.
                                                                                     Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised HFE7A designed heavy chain protein #2.
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                                                                                                                                                                                                                                               cells with abnormal Fas-Fas ligand systems
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                                                                                       Nakahara K,
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98JP-0276882.
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                                                                                       Serizawa N, Haruyama H,
                                           (SANY ) SANKYO CO LTD.
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Matches 34; Conserval
                                                                                                                              WPI; 2000-258930/23.
                                                                                                                                                       N-PSDB; AAA11597
30-SEP-1998;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apptosis in cells with a normal system, by inhibiting binding between the apoptosis in cells with a normal system, by inhibiting binding between the products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, anti-anemic, nephrotropic, antimosuppressive, thyromimetic, antirheumatic, nephrotropic, antimosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce cappoptosis by binding to cell surface Fas or inhibit it by competitive contains associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic cupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft or unuliple solerosis, Bashimoto disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEF7A designed heavy chain which is used in the invention.
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Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example reference 22; Page 150-152; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory or autoimmune disease, induces
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Matches 34; Conserv
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                                                                                                                                                                                                                                                                  Synthetic.
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This introduced apoptosis in cells with an abnormal Fas/Fas molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by indibiting binding between the apoptosis in cells with an abnormal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-amemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, antidiabetic, antidiabetic, antinfertility, enventorior antidiabetic, antidiabetic, antidiabetic, antidiateriors products of immunoaculatory dermatological, immunosuppressive, thyromimetic, antidiateriorsclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic compania, bost disease, soleroderma, Goodpasture syndrome, Crohn's disease, solorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively indiat apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunowodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antirhematic; anti-Fas; nephrotropic; antilnfertility; neuroprotective; antifarteriosclerotic; hepatotropic; antilnfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                  AAW90933 standard; Protein; 470 AA
110 tavyycarnrdysnnwyfdv 129
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98JP-0276882.
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inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                   100.0%; Score 246; DB 21; Length 470;
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                                                                                                                                                    4.1e-10
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46; Mismatches
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                                                                                                                                                                                                                                                                                                           110 tavyycarnrdysnnwyfdv 129
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98JP-0276882.
                                                                                                                                                        42.58;
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                                                                                                                                                                          34; Conservative
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                                                                                                                                                        Sest Local Similarity
                                                                              470 AA;
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30-SEP-1998;
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
disease, sociated with the Fas/Fas ligand system, especially systemic
c upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, soleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
antipibe sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetos mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CE, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-Fas antibody heavy chain construct designated Heu 2.
which is described in the method of the invention.
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46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0307711.
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW90935;
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g ò Search completed: August 14, 2002, 15:15:33

Job time: 831 sec

61 XXXXXXXXNRDYSNNWYFDV 80

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This invention describes a novel numbrized anti-ras anticody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas [1gand system, by binding to Fas on the cell surface, and prevents capoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive confinition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic confinition of ligand binding. (I) are used to treat and/or prevent disease, solorgen's syndrome, pernicious or hypoplastic conemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolyfic anemia, sterility, myasthenta gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively (B, C or D) or alcoholic), and transplant rejection. (I) selectively (I) the native ligand, do not induce liver disease, and have reduced risk of the native ligand, do not induce liver site of Fas, i.e. they mimic inducing a human anti-murine antibody response. This sequence represents a humanised anti-marine antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
                                                                                                   New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 246; DB 21; Length 470; 42.5%; Pred. No. 4.1e-10; ive 46; Mismatches 0; Indels 0
                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                    Claim 2; Page 180-182; 263pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 34; Conservative
                      WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.0 AA;
                                                   N-PSDB; AAA11646.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:05:37 ; Search time 82.88 Seconds (without alignments) 23:577 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table:

231628 segs, 24425594 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched: 231628

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score 176	Query Match 71.5	Len	DB - 2	US-08-553-497A-12	8, 12,	Appli Appl
	164 164	66.7 66.7 66.7	111	m m m	US-08-881-037-14 US-08-881-037-16 US-08-881-037-61	16,	Appl Appl Appl
	164	65.0	1119		US-08-881-037-62 US-08-881-037-17	62,	Appl Appl
	159 159	64.6 64.6		m m +	US-08-881-037-63 US-08-881-037-59 US-08-235-838-11		Appl Appl
	157.5	64.0		121	US-08-465-473B-11 US-08-235-838-16	11, 16,	Appl Appl
	157.5 157 157	64.0 63.8 63.8		01 m m	US-08-465-473B-16 US-08-881-037-15 US-08-881-037-60	Sequence 16, Sequence 15, Sequence 60, Seque	Appl Appl Appl
	155 155	63.0		ოო	US-09-027-449-48 US-09-027-449-49	48,	Appl Appl
	155 155	63.0		ოო	US-08-804-444A-48 US-08-804-444A-49	48,	Appl Appl
	155 155	63.0 63.0		4 4	US-09-026-985-48 US-09-026-985-49	48,	Appl Appl
23	147.5	60.09			US-08-398-613A-50 US-08-398-612A-50	50,	Appl Appl
	147.5	60.09	135 135	7	US-08-398-611A-50 US-08-491-334A-50	50, 50,	Appl Appl
	147.5	60.09		ოო	US-09-027-449-37 US-08-804-444A-37	37,	Appl Appl

Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
37,	58,	58,	58,	58,	44,	52,	55,	44,	52,	55,	44,	52,	55,	70,	70,	60,	90
Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-026-985-37	US-08-398-613A-58	US-08-398-612A-58	US-08-398-611A-58	US-08-491-334A-58	US-09-027-449-44	US-09-027-449-52	US-09-027-449-55	US-08-804-444A-44	US-08-804-444A-52	US-08-804-444A-55	US-09-026-985-44	US-09-026-985-52	US-09-026-985-55	US-09-027-449-70	US-09-026-985-70	US-09-027-449-60	US-08-804-444A-60
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135	253	253	253	253	253	253	253	253	253	253	253	253	253	256	256	298	298
0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09
147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5	147.5

## ALIGNMENTS

RESULT

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amino acid
                   TOPOLOGY:
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                                                                                                                                                                                                                                                     APPLICANT: ADAM, JANUES
APPLICANT: NITJANS, FRANSESC
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: ROSELL, ELISABET
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                 Query Match 71.5%; Score 176; DB 2; Length 119; Best Local Similarity 31.6%; Pred. No. 8.1e-07; Matches 25; Conservative 50; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/05/53,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION NUMBER: EP 94118970.6
FILING DATE: 17-MAR-1994
ATONNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,3022,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08553497A Patent No. 5844093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KETTLEBOROUGH, C. A
BENDIG, MARY M.
ANSELL, KEITH H.
GUSSOW, DETLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              91 SAVYYCARS-DYGSS-HFD 107
                                                                                                                                                                                                                                                                                                                                      61 XXXXXXXXNRDYSNNWYFD 79
                   : 119 amino acids
amino acid
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SEQUENCE CHARACTERISTICS
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                                                                              MOLECULE TYPE: protein
                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22201
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-08-553-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                        TOPOLOGY:
                                                                                                    US-08-553-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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Gaps
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                                                                                                                 Length 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OURTHAING SISTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION NUMBER: US/08/481,540
FILING DATE: 3-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: US 08/443,540
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 813-5600
TELEPAX: (650) 8494-0792
                                                                                                            Query Match 71.5%; Score 176; DB 2; Best Local Similarity 31.6%; Pred. No. 8.1e-07; Matches 25; Conservative 50; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 164; DB 3;
30.0%; Pred. No. 7.7e-06;
Live 46; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Glick, Gary D.

APPLICANT: Swanson, Patrick C.

TITLE OF INVENTION: DNA BINDING ANTIBODIES

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-881-037-14; Sequence 14, Application US/08881037; Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                       91 SAVYYCARS-DYGSS-HFD 107
                                                                                                                                                                                                                                                                                                              61 XXXXXXXXNRDYSNNWYFD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.7%
Best Local Similarity 30.0%
Matches 21; Conservative
                 ; MOLECULE TYPE: protein US-08-553-497A-12
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
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1 SYWMQXXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                              COMPUTER: IBM PC_COMPATIBLE
COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/881,037
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 66.7%; Score 164; DB 3; 1
Best Local Similarity 30.0%; Pred. No. 9.5e-06;
Matches 21; Conservative 46; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOEIST.
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-WAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                        ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 SAVYYCAKGR 100
                                                                                                     COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 XXXXXXXNR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1018
                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-881-037-61
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US-08-881-037-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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30.0%; Pred. No. 7.7e-06;
Live 46; Mismatches 3; Indels
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COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/O8/881,037

TILING DATE: 23-JUN-1997
                                                                                                                                  Sequence 16, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INFURION: DNA BINDING ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAX-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/08881037 Patent No. 6080588 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-881-037-16
                          83 SAVYYCAKGR 92
61 XXXXXXXXNR 70
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                                                                                                 RESULT 4
US-08-881-037-16
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US-08-881-037-61
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                                                                                                                                                                                                                                                                                        Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KOGISTATION: MALGINETE F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 160; DB 3; I.
29.0%; Pred. No. 2.1e-05;
iive 46; Mismatches 3;
                                                                                                                                                                                                                                                                                     65.0%; Score 160; DB 3; ilarity 29.0%; Pred. No. 1.7e-05; Conservative 46; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
APPLICANT: Swanson, Day Bunding ANTIBODIES NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203442110710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 755 Page Mill Road CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-881-037-63
; Sequence 63, Application US/08881037
; Patent No. 6080588
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                               LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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Best Local Similarity 29.0°
Matches 20; Conservative
   INFORMATION FOR SEQ ID NO:
                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conserva
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STRANDEDNESS: si
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                                                                                                                                                                linear
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US-08-881-037-17
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SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.7%; Score 164; DB 3;
Best Local Similarity 30.0%; Pred. No. 9.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Mismatches
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KOOSKI, ANTOINETHE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: MOILISON & Foerster STREET: 755 Page Mill Road CITY: Palo Alto STATE: CA COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid STRANDEDNESS: single
FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
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US-08-881-037-62
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US-08-881-037-17
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TELEX:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-300-1997
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Glick, Gary D.
APPLICANT: SAMORON, BALFICK C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STREET: GA
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFCATION 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/ABENT INFORMATION:
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-5600
TELECOMMUNICATION 18-5600
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Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
                                                                                                                                                                                              Sequence 59, Application US/08881037
Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59:
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SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
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Matches 20; Conserve
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                                                                                               92 AVYYCAKGR 100
                                                       62 XXXXXXXNR 70
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US-08-235-838-11
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US-08-881-037-59
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                                                           APPLICANT: ZWICKLI, MATKUS
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
SOGTWARE: Patentin Release #1.0, Version #1.25
SOGTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGBWT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
MATERIAL JAMES AS A SOUTH
TELECOMMUNICATION NUMBER: 36,129
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; Pred. No. 0.00031;
47; Mismatches 10;
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APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
                       Groner, Bernd
Hardman, No. 5571894man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-465-473B-11
Sequence 11, Application US/08465473B
Patent No. 5939531
GENERAL INFORMATION:
Harwerth, Ina-Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 SAVYYCAKG-GASGDWYFDV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.0%;
Best Local Similarity 27.5%;
Matches 22; Conservative 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 XXXXXXXXNRDYSNNWYFDV 80
                                                                                                                                                                                                                     7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-235-838-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                               CITY: Hawthorne STATE: New York
                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                              ADDRESSEE:
STREET: 7
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63 SYWMINYVRQRPGQGLEWIGMIDPSDSETQYNQMFKDKAALTVDKSSNTAYMQLSSLTSED 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wels, Winfried S.
APPLICANT: Wels, Mancy E.
APPLICANT: Horwerth, Ina-Maria
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Hardman, No. 5939531man
APPLICANT: Arickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSBE: NOVARTIS CORPORATION
STREET: 564 MORRIS AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 564 MOLLAL-
STREET: 564 MOLLAL-
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/465,473B
TIING DATE: 5 June 1995
                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,838

FILING DATE: TBA

CLASSIFICATION A435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/828,832

FILING DATE: 31-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 91-810079.3

FILING DATE: 05-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 4-18518/A/CIP/CONT

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ 1D NO: 16:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.0%; Score 157.5; DB Best Local Similarity 27.5%; Pred. No. 0.0058; Matches 22; Conservative 47; Mismatches 1
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08465473B Patent No. 5939531 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 SAVYYCAKG-GASGDWYFDV 141
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  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 637 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-235-838-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
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Fatent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Armony, No. 5571894man
APPLICANT: Zwick! Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                            MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/828,832
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
REGISTRATION NUMBER: 22,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.0%; Score 157.5; DB 2; Best Local Similarity 27.5%; Pred. No. 0.00031; Matches 22; Conservative 47; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIBA-GEIGY Corporation
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAVYYCAKG-GASGDWYFDV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h: 7 Skyline Drive
Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                    Summit
New Jersey
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                                                                                                                                     ZIP: 07901-6940
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STREET: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-465-473B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                            STATE: N
COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                              1 SYWMQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX 60
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Best Local Similarity 27.1%; Pred. No. 4e-05;
Matches 19; Conservative 48; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/881,037 FILING DATE: 23-JUN-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/443,540 FILING DATE: 18-MAY-1995
                                                                                                                                                                                                  Score 157; DB 3;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Gary D.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORIBOON & FOERSER:
ADDRESSEE: MORIBOON & FOERSER:
CITY: Palo Alto
                                                                                                                                                                                                                                                48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-881-037-60
; Sequence 60, Application US/08881037
; Patent No. 6080588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                Query Match 63.8%;
Best Local Similarity 27.1%;
Matches 19; Conservative 41
                                    LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 494-0792
              SEQUENCE CHARACTERISTICS:
                                                                             ESS: single
linear
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MEDIUM TYPE: Floppy
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                               83 SAVYYCAKGR 92
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                                                                                                          ; TOPOLOGY:
US-08-881-037-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PILING DATE: 23-UNN-1997
FILING DATE: 23-UNN-1997
FILING DATE: 23-UNN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.0%; Score 157.5; DB 2; 27.5%; Pred. No. 0.0058; tive 47; Mismatches 10;
                                                                                                                                                                                                                     4-18518/A/CIP/CONT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:

APPLICATION NUBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTATION NUBER: 22,640
REFERENCE/DOCKET NUBER: 4-18518/A/CI
TELEPHONE: (908)522 6940
TELEPHONE: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: MINIOR ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KONSKİ, ANCOINETE:
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 2034421107:
TELECOMUNICACION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SAVYYCAKG-GASGDWYFDV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 XXXXXXXNRDYSNNWYFDV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 27.59
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-473B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-881-037-15
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31 SYWIHWVKQRPGQGLEWIGEIDPSDNYTYYNQKFKGKATLTVDKSSSTAYMQLSSLTSED 90 g

61 XXXXXXXNR 70 :::::::| 91 SAVYYCAKGR 100

oy ob

Search completed: August 14, 2002, 15:17:02 Job time: 685 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:07:32 ; Search time 108.64 Seconds (without alignments) 70.758 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

2_G_3_G_4 246 1 SYWMQXXXXXXXXXXXXXXXE.....XXXXXXXXXNRDYSNNWYFDV 80

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283138 segs, 96089334 residues Searched:

283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Jel 1	ln V r	in V r	ln V r	Ln V r	in V r	ln V r	in V r	ln V r	ln V r	in V r	Ln (my	•	in V r	in V r	in V r	in V r	in pre	in V r	in V r	in V r	in V r	in pre	in V r	in V r				
	ion	Fab	chain	chain	chain	chain	chain	chair	chain	cha	cha																			
	Description	antibody	heavy																											
	Des	ant	Ig	Ig	Ig	Ig	Ιg	Ig	Ιĝ	Ig	Ig	Ιg	Ιđ	19	Ιg	Ιg	Ιg	ь		Б		19	6		Ιg	Iq	Ιđ	Ιđ	Ιđ	Ig
RIES																														
SUMMARIES	QI QI	S53751	PH1160	S26463	PH1162	PH1161	PL0089	B22769	PL0086	S41394	PH1426	S25175	S20643	н37262	D25150	MHMS4E	T01407	C30560	PH1004	PH1005	MHMS15	MHMSJ5	HVMS02	S24287	S20646	PH1521	B30560	A27472	B47159	PH0987
	DB	~	~	7	7	7	7	~	7	~	7	7	7	~	~		~	~	7	7	Н	Н	Н	~	7	~	~	7	7	7
	Length	116	86	111	87	88	119	120	119	120	122	120	122	101	69	117	140	118	91	106	120	117	117	122	123	119	123	131	136	107
ф	Query Match	76.4	68.7	68.1	7	ဖ	o.	65.2	ഹ	マ	64.6	62.2	61.8	61.4	61.0	61.0	61.0	9.09	60.2	0.09	0.09	59.3	ထ	œ	œ	œ	58.5	œ	œ	ထ
	Score	188	169	167.5	165	163	163	160.5		159.5	159	153	152	151	150	150	150	149	148	147.5	147.5	146	145	4	145	144	14	m	43	143
	Result No.	1	0	m	4	'n	9	7	œ	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

δ qq RESULT PH1160

Igheavy chain V region (clone 7A.1) - mouse (fragment)

C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: No.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C.Accession: PH1160
R.Schittek, B.; Rajewsky, K.
A.Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A.Reference number: PH1105; MUID:92364545
A.Accession: PH1165
A.Accession: PH1166
A.Residues: 1-98 «SCH»
A.Residues: 1-98 «SCH»
A.Residues: 1-98 region; immunoglobulin homology
C.Superimental source: B cell
C.Superfamily: immunoglobulin homology < Immunoglobulin homology
F;15-98/Domain: immunoglobulin homology < IMM>

68.7%; Score 169; DB 2; Length 98; 30.9%; Pred. No. 2e-05;

Query Match Best Local Similarity

30	143	58.1	118	77	A2	A24754	heavy chain V	
32	141.5	57.5	101	N (	r Hd		chain V	
33	141	57.3	86	7	PH		heavy chain V	
34	140.5	57.1	137	2	PH		heavy chain V	
35	140	0.0	102	~	Hd		heavy chain V	
9 10	140	000	114	N (	E .	PH1522	heavy chain v	
38	140	0. o.	110	3 0	E 6		heavy chain v	
0 0	0 7 1	. 0	110	10	. H		heavy chain V	
40	140	56.9	119	7	H		chain V	
41	140	56.9	119	7	PH		heavy chain V	
42	140	56.9	119	7	PH		heavy chain V	
43	140	56.9	119	7	ЬН		heavy chain V	
44 45	140 140	56.9	138	2 2	PH	PH1520 PH1565	lg heavy chain v r Ig heavy chain v r	
						ALIGNMENTS		
RESULT	1							
antibody	antibody Fab Jel 103 heavy chain	103 he	avv ch	air		- mouse		
C; Specie C; Date:	C;Species: Mus musculus (house mouse) C;Date: 23-Aug-1995 #sequence_revisio	nnsculus 1995 #se	opone duence	se n	ous vis	.lus (house mouse) #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999	ange 17-Mar-1999	
C; Accession:	ion: S5	S53751					,	
R; Pokkul	R;Pokkuluri, P.R.; Bouthillier, T Mol Biol 243 283-297 1994	8.; Bout	Bouthillier, 383-297 1994	994		F.; Li, Y.; Kuderova, A.; Lee,	ee, J.; Cygler, M.	
A; Title: A; Refere	Aritle: Preparation, characterization and A. Reference number: \$53750; MUID:95018269	ttion, c	haract 750; N	eri	zat ):95	ion and crystallization of 018269	of an antibody Fab fragmen	uei
A; Access	A; Accession: S53751	3751 11paru						
A; Molecu	A; Molecule type: mRNA	mRNA						
A; Residu C; Superf	A;Residues: 1-116 <pok> C;Superfamily: immunoglobulin V region;</pok>	l6 <pok> ummunogl</pok>	obulir	> .	reg		logy	
F;15-98/	15-98/Domain: immunoglobulin homology	immunog	lobuli	5	OIIIO	logy <imm></imm>		
Query Match Best Local Matches 2	Query Match Best Local Similarity Matches 25; Conser	76. nilarity 32. Conservative	vat	76.4%; 32.9%; ive	47	Score 188; DB 2; Length 116; Pred. No. 5.5e-07; 47; Mismatches 4; Indels	116; ls 0; Gaps 0;	
Oy Db 3	1 SYWMQN	KXXXXXX ::::::: IVKQRPGQ	XXXXX	KEIL	PSD 	SYMMQXXXXXXXXXXXXXXEIDPSDSYTNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	XXXXXXXXXX 60 ::::::::::: MQLSSLTSED 90	

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Query Match
Best Local Similarity
Matches 21; Conserv
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Matches 22; Conserv
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                                                                                                                                                                                                                   526463
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan.1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ig heavy chain V region (clone 10C.2A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1162
R;Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1192
A;Fille: Natural occurrence and origin of somatically mutated memory B cells A;Reference number: PH1105; MUID:92364545
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                                    SYMMOXXXXXXXXXXXXXXXX EIDPSDSYTNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 < KAV>
A;Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology < IMM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 6-87/Domain: immunoglobulin homology <IMM>
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   Indels
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 Mismatches
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                                                                                                                                                                                                                                                                                                                R; Kavaler, J. submitted to the EMBL Data Library, April 1991 A; Reference number: $226459 Accession: $20465
 47;
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Best Local Similarity
Matches 23; Conserv
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Matches 21; Conserv
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A; Residues: 1-87 <SCH>
                                                                                                                                               86
                                                                                                          89 XXXXXXX
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                                                                                                                                               SAVYYCAR
21;
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C. Accession: PL0089
R. Meek, K.: Hasemann, C.: Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.;
R. Meek, K.: Hasemann, C.: Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.;
R. Exp. Med. 169, 519-533, 1989
A. Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s
A. Recession: PL0089
A. Mocession: Mocession: Mocession: Mocession and A. Mocession and 
                                                                                                                                                                                                                                                                                                                      somatically mutated memory B cells in mice.
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                                      C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Date: 30-5ep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C'Accession: PH1161
R'Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 11992
A'STILE: Natural occurrence and origin of somatically mutated memory B cells A'Reference number: PH1105; MUID:92364545
A'Recession: PH1165
A'Recession: PH1167
A'Recession: PH1168
A'Recession: H188 <SCH>
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C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (12518-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 7-88/Domain: immunoglobulin homology <IMM>
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chain V region (clone 13B.2A) - mouse (fragment)
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A;Cross-references: EMBL:X67620; NID:951856; PIDN:CAA47878.1; PID:9938260 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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24.4%; Predictive 53;
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29.1%;
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Best Local Similarity 29.1%
Matches 23; Conservative
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Best Local Similarity
Matches 19; Conserv
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A; Residues: 1-120 <MON>
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              A;Status: preliminary
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Through the second of the seco
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541394
19 heavy chain V region - mouse
() Species: Mus musculus (house mouse)
() Species: Mus musculus (house mouse)
() Species: Mus musculus (house mouse)
() Accession: 841394
() R. Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
Submitted to the EMBL Data Library, January 1994
A) Reference number: S41393
A) Reference number: 841393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 SYWMQWVKQRPGRGLEWIGDIYPGDGYARYTQKFKAKATLTADKSSSTAYMQLSSLASED 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SYWMQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.0%; Score 160; DB 2; 26.2%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 160.5; DB 2
Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       65.2%;
29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 XXXXXXXNRDYSNNWYFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Conservative
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nes 21; Conserv
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Best Local S:
Matches 21,
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A; Note: the authors translated the codon AAA for residue 28 as Ser and GTA for residu
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J. Exp. Med. 177, 99-107, 1993
A; Title: Molecular evolution of the human immunoglobulin E response: High incidence
                                                                                                                                                                                                                                                                                                                              1;
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A; Molecule, type: mRNÅ
A; Residues: 1-120 < CMAR>
A; Residues: 1-120 < CMAR>
A; Cross-references: EMBL:229586; NID:9452354; PIDN:CAA82703.1; PID:91334080
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibodies to
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                1 SYWMQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     31 SYWMHWYKQRPGQGLEWIGEIDPSDSYTYYNQKFKGKATLIVDKSSSTAYMQFSSLTSED 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYWMQXXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
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submitted to the EMBL Data Library, July 1992
A; Description: Structure and binding properties of monoclonal ant
A; Reference number: S25174
A; Accession: S25175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone P2-57) - human (fragment)
                                                                                                                                                                                                                                                             ; Score 159.5; DB 2;
; Pred. No. 0.00018;
47; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 159; DB 2;
Pred. No. 0.00021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: immunogrouns...
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: PH1409; MUID:93115676
A; Accession: PH1426
A; Molecule type: mRNA
A; Residues: 1-122 </a>/AN>
A; Experimental source: PBMC
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C. Accession: A02039
B. Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
B. Biochemistry 21, 5415-5424, 1982
B. Reference number: A02039; MUID:83075344
A. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
A. Accession: A02039
B. Reference number: A02039; MUID:83075344
C. Comment: The group and a sequence of a mouse mu chain: homology among heavy chain
B. Residues: 1-117 ckEH>
C. Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context C. Comment: This protein binds dextran.
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: glycoprotein; heterotetramer: immunoglobulin predicted
C. Keywords: glycoprotein; heterotetramer: immunoglobulin predicted
F. 15-96/Domain: immunoglobulin bomology cIMM>
F. 12-96/Disulfide bonds: #status predicted
F. 15-Binding site: carbohydrate (Asn) (covalent) #status atypical
                                                                                                                                                                                                                                                                                                ig heavy chain V region (AC38 260.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996
C;Accession: D25150
R;Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
BMBO J. 3, 517-523, 1984
A;Title: A V region determinant (idiotope) expressed at high frequency in B lymphocyt
A;Reference number: A91000; MUID:84182519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SYWMNWIKQRPEQGLEWIGRIDPYDSETHFNQXFKDKALLIVDKSSSTAYMQLSSLTSED
        1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-69 <DIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 150; DB 2;
41.2%; Pred. No. 0.00053;
iive 29; Mismatches 1.
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25.3%; Pred. No. 0.0012;
live 53; Mismatches 2
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                                                                                                               61 XXXXXXXXNRDYSNNWY 77
                                                                                                                                                    83 SAVYYCARSYDYLPPWF 99
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
Matches 21; Conserv
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R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A,Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: H37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
B;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
A;Title: Common structural features among monoclonal antibodies binding the same antiger
A;Reference number: A38601; MUID:91115823
A;Accession: H37262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (2F8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
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                                                                                                                                                                                            Gaps
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                                                                                  Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                               62.2%; Score 153; DB 2; L
26.8%; Pred. No. 0.00068;
ive 49; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 152; DB 2;
Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                     91 SAVFYCAREKITDDYN---YFD 109
                                                                                                                                                                                                                                                                                                      61 XXXXXXXNR---DYSNNWYFD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 61.8%;
1 Similarity 25.4%;
18; Conservative 4
                                                                               Query Match 62.2%
Best Local Similarity 26.8%
Matches 22; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-122 <LOS>
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A; Residues: 1-101 <GOS>
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Gaps

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Indels

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2002, 15:11:47; Search time 53.64 Seconds (without alignments) 57.747 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

2_G_3_G_4
246
1 SYWMQXXXXXXXXXXXXXXXX

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	mus		mus	P01750 mus musculu	P01747 mus musculu	P01751 mus musculu	P03980 mus musculu	gnm 9	Snm 6	mus	P06330 mus musculu	P01748 mus musculu	P01753 mus musculu	P01754 mus musculu	P06328 mus musculu	P01812 mus musculu	P01808 mus musculu	P01811 mus musculu	P01759 mus musculu	P01809 mus musculu	P01755 mus musculu	P23083 homo sapien	P23667 xenopus lae	P01743 homo sapien	_	P06327 mus musculu	P01807 mus musculu	P01793 mus musculu	P01741 mus musculu	P01787 mus musculu	)5 ratt	5 mus	P01806 mus musculu
SOMMAKIES	QI	HV12_MOUSE	HV50_MOUSE	HV13_MOUSE	HV06_MOUSE	HV03_MOUSE	HV07_MOUSE	HV48_MOUSE	HV02_MOUSE	HV05_MOUSE	HV01_MOUSE	HV51_MOUSE	HV04_MOUSE	HV09_MOUSE	HV10_MOUSE	HV49_MOUSE	HV42_MOUSE	HV38_MOUSE	HV41_MOUSE	HV15_MOUSE	HV39_MOUSE	HV11_MOUSE	HV1G_HUMAN	CO3_XENLA	HV1B_HUMAN	HV40_MOUSE	HV52_MOUSE	HV37_MOUSE	HV24_MOUSE	HV00_MOUSE	HV18_MOUSE	HV01_RAT	HV26_MOUSE	HV36_MOUSE
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	Length	117	120	117	117	120	139	138	140	117	121	118	117	117	117	117	117	119	117	136	118	137	117	323	117	119	117	119	123	114	123	142	144	911
& Query		Н	0.09	σ.	œ	o	9	4	◂	m	a	$\overline{}$	0	0	0	0	σ	9	45.1	4	4	4		4	m	43.5	2	42.7	$^{\circ}$	2	S	N	42.1	41.9
	Score		147.5	146	145		139.5	m	133	132		125.5	125	124	124	124	121	113.5	111	110	109.5	109.5	109	108.5	108	107	105		104.5	104	103.5	103.5	103.5	103
Result	Š.	7	7	m ·	4	Ŋ	9	7	80	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

RESULT 2
HV50_MOUSE
TO HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 12-JUL-1999 (Rel. 38, Last annotation update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 heavy chain V region AC38 15.3.

222224222											,; ,;		
P01789 mus musculu P30193 staphylococ P44764 haemophilus P01784 mus musculu P01791 mus musculu P87023 candida alb Q01663 schizosacch P1746 homo sapien P53052 yersinia en P32486 saccharomyc				Euteleostomi; ; Murinae; Mus.	Sibley C.H.,	homology among	DF THIS IGM MYELOMA			54;	ngth 117; Indels 4; Gaps	XXXXXXXXXXXX 61	
HV20_MOUSE EPPI2_STAEP CN16_HAEIN HV19_MOUSE HV22_MOUSE HV23_MOUSE API_SCHPO DPPO_ESST API_SCHPO CN16_YEAST CN16_YEAST KRE6_YEAST	ALIGNMENTS	PRT; 117 AA.	Created) Last sequence update) Last annotation update) on MOPC 104E.	Craniata; Vertebrata; Sciurognathi; Muridae	16276; chilling J.W., Rogers J.,	e mu chain:	24 (1982). SEQUENCE OF THE LIGHT CHAIN OF EN DETERMINED. PROTEIN BINDS DEXTRAN.		Glycoprotein. BY SIMILARITY. N-LINKED (GLCNAC).	N; 3CF8ACE4BE447E41 CRC64	Score 150; DB 1; Length Pred. No. 0.00043; 53; Mismatches 2; Inde	YWWQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	10
41.9 122 1 41.9 275 1 41.7 657 1 40.9 123 1 40.4 740.4 740.2 1 40.2 1097 1 39.6 652 1		STANDARD;	986 (Rel. 01, Created) 986 (Rel. 01, Last seg 999 (Rel. 38, Last ann chain V region MOPC 1	(Mouse). etazoa; Chordata; theria; Rodentia; 0090;	[1] SEQUENCE. MEDLINE-83075344; PubMed-6816276; Kehry M.R., Fuhrman J.S., Schilling	"Complete amino acid sequence of heavy chain constant region doma.	5-54 FHE D BE FHIS	MHMS4E. R003006; IG_MHC R003596; IG_V. 7; ig; 1.	1. ion; 96 55	117 1 17 AA;	h Similarity 25.3%; 20; Conservative	WMQXXXXXXXXXXEIDP( : ::::::::::::  YMKWVKQSHGKSLEWIGDINP	XXXXXXXNRDYSNNWYFDV 80 ::::::     :      AVYYCARDYDWYFDV 106
34 103 35 102.5 37 101.5 38 100.5 39 99.5 41 99.5 44 97.5 45 97.5		RESULT 1 HV12_MOUSE ID HV12_MOUSE	21-JUL-1986 21-JUL-1986 15-JUL-1999 Ig heavy cha	s musc karyot mmalia BI_Tax	[1] SEQUENCE. MEDLINE-83075344; Pubmer Kehry M.R., Fuhrman J.S.	"Complete am heavy chain	Blochemistry 21:541 -!- MISCELLANEOUS: PROTEIN HAS ALS -!- MISCELLANEOUS:	PIR; A02039; MHMS4E. InterPro; IPR003006; InterPro; IPR003596; Pfam; PF00047; ig; 1	SMART; SM00406; Immunoglobulin DISULFID 22 CARBOHYD 55	NON_TER SEQUENCE 1	y Match Local Simi nes 20;	2 YWMQXXX  : :::: 32 YYMKWVK	62 XXXXXXX ::::: 92 AVYYCA-
		RESUI HV12		800x	R R R R	1	₹888	DR DR	KW FT	FT SQ	Query Best Matcl	Qy Db	Qy Db

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Gaps

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SEQUENCE.

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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR; AD0323: HWMSO2.
InterPro; IPR003006; Ig_MC.
                                                                                                     2 YWMQXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX 61
                                                                                                                                                    32 YYMKWVKQSHGKSLEWIGDINPNNGGTSYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CS7BL/6;
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mús musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING - 1. FRAMEWORK - 2.
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                            22.8%; Pred. No. 0.00094;
Live 54; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 102. FRAMEWORK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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BY SIMILARITY.
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                            Best Local Similarity 22.8%
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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P01747;
                                                                                                                                                                                                                                                                                                                                                                                   HV06_MOUSE
P01750;
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HV06_MOUSE
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                                                                                                                                                                         MEDLINE-84182519; PubMed-6201362;
MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR: A02037; MHMS15.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM0046; IGv.
Immunoglobulin V region.
DOMAIN
1 98 V SEGMENT.
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OF
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 147.5; DB 1; Length 120; 25.0%; Pred. No. 0.00073; tive 50; Mismatches 9; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13311 MW; 914453F426F09834 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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INTERPO: IPR003006; Ig_MHC.
INTERPO: IPR003596; Ig_V.
INTERPO: IPR003596; Ig_V.
INTERPO: IPR0047; Ig; I.
SMART; SM00406; IGV: I.
Immunoglobulin V region.
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Matches 20; Conservative
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120 AA;
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HV13_MOUSE P01757;

HV13_MOUSE

RESULT

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SEQUENCE

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Query Match

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ö Gaps 1 SYWMQXXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXX 60 ó Query Match 58.9%; Score 145; DB 1; Length 117; Best Local Similarity 26.5%; Pred. No. 0.0011; Matches 18; Conservative 46; Mismatches 4; Indels 12867 MW; 740A65DD851FCA8C CRC64; (Rel. 01, Created) (Rel. 01, Last sequence update) (Rel. 38, Last annotation update) 21-JUL-1986 ( 21-JUL-1986 ( 15-JUL-1999 (

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Query Match

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15576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     109 DSAVYYCARYDYYGSSYFD 127
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PIRE, A02033; HWAT7.
INTERPRO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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138
138 AA;
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Best Local Similarity
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HV48_MOUSE
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                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                         The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                   idiotype response of the strain A mouse.";

Eur. J. Immunol. 12:1023-1037(1982).

-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
Ig heavy chain V region 36-65.
Was musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                 Ouery Match 56.9%; Score 140; DB 1; Length 120; Best Local Similarity 20.3%; Pred. No. 0.0032; Matches 16; Conservative 53; Mismatches 10; Indels
                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
NON TER
SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                     MEDLINE-83131846; Pubmed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
HV07_MOUSE
D 10751, P01752,
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 heavy chain V region B1-8/186-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                         PIR; A02028; HVMGG7.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 SAVYFCARSVYYGGSYYFD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 XXXXXXXXNRDYSNNWYFD 79
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                                                                                                              Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEGMENT, JH2.
                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Illegitimate recombination generates a class switch from C mu to C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.7%; Score 139.5; DB 1; Length 139; 22.8%; Pred. No. 0.0046;
                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                  139 JHZ SEGMENT.
115 BY SIMILARITY.
139 IS419 MW; 1B57DD4FDOC9F465 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V region TEPC 1017 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Mismatches
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                                                                                                                                                                                                                                                                                                                                     FRAMEWORK-3.
D SEGMENT.
JH2 SEGMENT.
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                                                                                                                                                                                                                                     FRAMEWORK-1
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EMBL; J00529; AAA38170.1; -.
PIR; AQ204; MHMS18.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PP00407; ig; 1.
SMART; SM00406; IGy; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84248078; PubMed=6429663;
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SMART; SM00406; iGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                     "Heavy chain variable region contribution to the NPD family of antibodies: sometic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANBOUGS THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 SYWMDHVKQRPGGGLEWIGNIYPSDSETHINQKFKDKATLIVDKSSSTAYWQLSSLISED 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                  MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.7%; Score 132; DB 1; Length 117; ilarity 23.5%; Pred. No. 0.015; Conservative 47; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13016 MW; 427C861C53975EDC CRC64;
                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                               Ig heavy chain V region 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
STANDARD;
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54
68
85
                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=10090;
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P01745;
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SEQUENCE
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DOMAIN
DOMAIN
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                                                                                                                                     50 SYGINWYKQRPGQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSED 109
                                                                          Gaps
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                                                                                                             Pfan, PF00047; 1g; 1. SMART; SM00406; 1Gv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                  Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION 93G7
                                                                          Indels
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                                                                  7;
                                  54.3%; Score 133.5; DB 1;
18.2%; Pred. No. 0.015;
iive 55; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=82152818; PubMed=6801765;
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PIR; A02028; HVMSG7.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 15; Conservative
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
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140 AA;
                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                  Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                                         HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capra J.D.;
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SEQUENCE
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HV02_MOUSE
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Baltimore D.,
"Heavy chain variable region contribution to the NPD family of
"Heavy chain variable region evident in a gamma 2a variable region.",
call 24:625-637(1981)
-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 SYWMHWYKQRPGQGLEWIGNINPGNGGTNYNEKFKSKYTLTVDKSSSTAYTQLSSLTSED 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                    61
                                      1 SYWWQXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CSTBAL/6;
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari I., Rajewsky K.,
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12772 MW; C530F829C906F69B CRC64;
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                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                        Ig heavy chain V region 23 precursor. Mus musculus (Mouse).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
FROM PF00047; Ig_v.
SMART; SM00406; IGv.
Immunoglobulin V region; Signal.
                                                                                                                      92 AVYYCARGYGYDP---FDV 107
                                                                                         62 XXXXXXXNRDYSNNWYFDV 80
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117 AA;
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ID HV04_MOUSE
AC P01748;
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HV09_MOUSE
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                                                                                                                                                                          Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MENA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes."; EMBO J. 3:517-523(1984).

PIR; A02040; MHMS38.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinell Lougo;
                                                  MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 52.8%; Score 130; DB 1; Length 121; 17.7%; Pred. No. 0.024; ive 53; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                          NON_TEŘ 121 121
SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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InterPro; IPR003506; Ig_MHC.
InterPro; IPR004596; Ig_v.
SMART; SW00407; Ig; 1.
Inmunoglobulin V region.
I 98 V
DOMAIN 105 118 D
DOMAIN 105 118 D
DOMAIN 22 96 B;
NON TER 118 AA; 12934 MW;
                                                                                                                                                                                                                                               PIR, A02027; GVMS11.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam: PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 SAIYHCARGIYYNSSPYFD 109
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Best Local Similarity 17.7%
Matches 14; Conservative
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Matches 16, Conservative
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                                   SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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P06330;
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REVISIONS.
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Query Match
Best Local Similarity
Matches 13; Conserv
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P06328;
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HV49_MOUSE
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                                                                                              "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:635-637(1981).
-i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                            FRAMEWORK - 1.
COMPLEMENTARITY - DETERMINING - 1.
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                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 186-1.
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                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                         12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV10_MOUSE STANDARD; PRT; 117 AA. P01754; P11270; 21-JUL-1986 (Rel. 01, Created) (01-JUL-1989 (Rel. 11, Last sequence update) (15-JUL-1999 (Rel. 38, Last annotation update) ig heavy chain V region 145 precursor.
                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                    FRAMEWORK - 2
                                                                                                                                                   PIR, B02034; HVMS61.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                     STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-81234548; PubMed-6788376;
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117 AA;
                                          SEQUENCE FROM N.A.
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                    NCBI_TaxID=10090;
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                                                                                     Baltimore D.;
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HV10_MOUSE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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"Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.4%; Score 124; DB 1; Length 117; ilarity 19.1%; Pred. No. 0.073; Conservative 48; Mismatches 7; Indels
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COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 145.
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15-JUL-1999 (Rel. 38, Last annotation update)
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19 19 IG H'
20 117 IG H'
                                                                                                                                                            PIR, C02034; HVMS45.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
InterPro: IPR003596; Ig_V.
SWART; SM00406; IGV.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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COMPLEMENTARITY-DETERMINING-1.	FRAMEWORR - Z. COMPLEMENTARITY - DETERMINING - 2.	JRK - 3.	BY SIMILARITY.		117 AA; 12834 MW; B8862FAC67ABD345 CRC64;	Query Match 50.4%; Score 124; DB 1; Length 117; Best Local Similarity 19.1%; Pred. No. 0.073; Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;	1 SYMMQXXXXXXXXXXXXXXXX EIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXX 60	50 SYWMHWYKQRPGRGLEWIGNIDPNSGGTKYNEKFKSKATLTYDKPSSTAYMQLSSLTSED 109		
54 COMPLEN	85 COMPLEMENTAR	117 FRAMEWORK-3.	115 BY SIMI	117	12834 MW; B8862	50.4%; Score 1 19.1%; Pred. N ative 48; Mism	XXXXXEIDPSDSYTNYN	LEWIGNIDPNSGGTKYN		
50 0 11	ກ	98	41	117	117 AA;	lmilarity : Conserv	XXXXXXXX	IWVKQRPGRO	89 XXX	:::: rctr 117
DOMAIN	DOMAIN	DOMAIN	DISULFID	NON_TER	SEQUENCE	uery Match West Local Si Tatches 13,	1 SYWM	50 SYWM	61 XXXXXXX 68	110 SAVYYCTR 117
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Search completed: August 14, 2002, 15:23:12 Job time: 685 sec

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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:10:52; Search time 187.61 Seconds (without alignments) 73.768 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

562222 Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

8: Sp_organolle:*
9: Sp_hage:*
10: Sp_lant:*
11: Sp_rodent:*
12: Sp_virus:*
13: Sp_vertebrate:*
14: Sp_unclassified:* 1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:* sp_rvirus:* sp_bacteriap:* sp_archeap:* 110 112 113 114 116 116 116

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	O91v67 mus musculu	mus	mus n	Q91wt3 mus musculu	mus	Q9j181 mus musculu	0924p5 mus musculu	_	mus 1	snu	mus	mus	mus	mus		
		1															
	DI	Q91V67	Q924P9	092402	Q91WT3	0924R3	Q9JL81	Q924P5	092405	Q9QXF0	Q924P8	Q921K1	Q924R8	092407	Q9JL77	092400	090XE9
	DB	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
	Query Match Length DB	143	143	142	481	145	114	144	143	117	140	278	146	145	110	143	117
#P	Query Match	75.8	71.1	64.8	64.8	64.4	0.09	59.3	58.3	58.1	57.7	57.1	56.9	26.7	55.5	55.1	54.5
	Score	186.5	175	159.5	159.5	158.5	147.5	146	143.5	143	142	140.5	140	139.5	136.5	135.5	134
	Result No.	-	7	æ	4	2	9	7	80	σ	10	11	12	13	14	15	16

Q924r7 mus musculu Q91va2 mus musculu Q924r4 mus musculu Q924r4 mus musculu Q924sr mus musculu Q925s2 mus musculu Q92y2 schistosoma Q92y2 schistosoma Q924r3 mus musculu Q924r5 mus musculu Q924r6 mus musculu Q924r1 mus musculu Q91wr1 mus musculu	uns nus nus nus nus nus
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44444741111111111111111111111111111111	109 143 298 116
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1117 2222 2222 2222 2233 2333 2333 2333	044444 0010845

# ALIGNMENTS

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RESULT

	; 143 AA.		(pe	sequence update)	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	VH186.2-D-J-C MU PROTEIN (V304-D-J-C MU PROTEIN) (FRAGMENT).		•	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						"Direct Estimation of Relative Affinity by Flow Cytometry Reveals	Affinity Maturation of B Cell Antigen Receptors in Response to (4-	Hydroxy-3-Nitrophenyl)Acetyl (NP).";	<pre>3enBank/DDBJ databases.</pre>					91BC6012B44EFEBF CRC64;	
	PRT;		Creat	Last	Last	04 - D-			; Cra	; Sci					. ;	ve Af	l Ant	(NP)	EMBL/		ŗ				
	PRELIMINARY;		(TrEMBLrel. 19, (	(TrEMBLrel. 19, 1	(TrEMBLrel. 19, 1	-C MU PROTEIN (V3(	MU.	s (Mouse).	Metazoa; Chordata	utheria; Rodentia	10000;		OM N.A.	L/6;	Kozono Y., Kozono H., Azuma T.;	imation of Relativ	turation of B Cel	itrophenyl)Acetyl	AUG-2001) to the 1	EMBL; AB069912; BAB63928.1;	EMBL; AB069914; BAB63930.1;	1 1	143 143	143 AA; 15775 MW;	
767	Q91V67	Q91V67;	01-DEC-2001	01-DEC-2001	01-DEC-2001	VH186.2-D-J	V304-D-J-C MU.	Mus musculus (Mouse).	Eukaryota; 1	Mammalia; E	NCBI_TaxID=10090;	[1]	SEQUENCE FROM N.A.	STRAIN-C57BL/6;	Kozono Y., 1	"Direct Est:	Affinity Mat	Hydroxy-3-N.	Submitted ()	EMBL; AB069!	EMBL; AB069	NON_TER	NON_TER	SEQUENCE	
091V67	ID	AC	占	텀	DŢ	DE	GN	SO	႘	ပွ	ŏ	RN	RP	2	RA	RT	RT	RT	RL	DR	DR	FT	FT	ÖS	

Gaps Query Match 75.8%; Score 186.5; DB 11; Length 143; Best Local Similarity 32.5%; Pred. No. 1.8e-05; Matches 26; Conservative 47; Mismatches 4; Indels 3;

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1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXXX 60 ò g

91 SAVYYCAPTVD---DWYFDV 107 61 XXXXXXXXNRDYSNNWYFDV 80 g

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0924P9 ~

RESULT Q924P9

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11 SYMMQWVKQRPGQGPEWIGEIDPSDIYTDYNQEFKGKATLTVDTSSSTAYMQLSSLTSED
                                                                                                                                                                                                                                     091WT3;
01-DEC-2001 (TFEMBLrel. 19, Created)
01-DEC-2001 (TFEMBLrel. 19, Last sequence update)
01-DEC-2001 (TFEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
HAND MUSCAULUS (MOUSE).
Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antique Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067787; BAB63272.1;
SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.8%; Score 159.5; DB 11; Length 481; Best Local Similarity 27.3%; Pred. No. 0.029; Matches 21; Conservative 50; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-COLON;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1; -.
Hypothetical protein.
evoireNCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186.2-5-7-C MU PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                    481 AA
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                                                                                                                 SAVYYCAR-RYYGGODYW 107
                                                                              61 XXXXXXXXNRDYSNNWYF 78
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                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
Matches 20; Conserva
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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SEQUENCE
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Q924R3
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                                                                                                                                                                                                                                                                                                                                                  Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP) ".
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB069916; BAB63932.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069910; BAB63926.1; -.
                                                                                                                                                                                                                  Mus musculus (Mouse),
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse),
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA; 15684 MW; 048809F90C0FBD7B CRC64;
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092402;
092402;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
V303-D-J-C MU PROTEIN (FRAGMENT).
V303-D-J-C MU.
                                                                                        0324P).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
v303-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.1%; Score 175; DB 11;
30.8%; Pred. No. 0.00014;
tive 50; Mismatches 4;
                                                                              143 AA
                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
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                                                                            PRELIMINARY;
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Best Local Similarity
Matches 24; Conserv
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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RESULT 092402

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Gaps

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Gaps 'n DB 11; Length 145; Indels 64.4%; Score 158.5; DB 11; 25.0%; Pred. No. 0.003; tive 48; Mismatches 11;

Query Match

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 1 SYWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXX 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEMENTAL CSTBL/6;
KOZONO Y., KOZONO H., AZUMMA T.;
KOZONO Y., KOZONO H., AZUMMA T.;
KOZONO Y., KOZONO H., AZUMMA T.;
FIDIECT ESTIDATION OF Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067795; BAB63280.1; -.
Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BabEl; AB069920; BAB63936.1; -.
NON TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinoae; Mu
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_raxID=10090;
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                                                                                                                                                                                                                                                                              DB 11; Length 144;
                                                                                                                                                                                                                                                                        59.3%; Score 146; DB 11; Length 1
24.7%; Pred. No. 0.028;
tive 49; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                     144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 AA; 15908 MW; 55A2372870F0D568 CRC64;
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01-MAY-2000 (TFEMBLrel. 13, Created)
01-MAY-2000 (TFEMBLrel. 13, Last sequence update)
01-DEC-2001 (TFEMBLrel. 19, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TIEMBLTE1. 19, Created)
01-DEC-2001 (TIEMBLTE1. 19, Last sequence update)
01-DEC-2001 (TIEMBLTE1. 19, Last annotation update)
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 SAVYYCAS---YGSSYWYFDV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 XXXXXXXNRDY-SNNWYFDV 80
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Best Local Similarity 23.8%
                                                                                                                                                                                                                                                                                                                                           20; Conservative
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                                                                                                                                                                                                                                                                                                              Similarity
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DB 11; Length 278;

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Kozono Y., Kozono H., Azuma T.; Affinity by Flow Cytometry Reveals affinity Maturation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Affinity Maturation of B Cell Antigen Receptors in Response to (4-Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB067781; BAB63266.1; --
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                         Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -
SEQUENCE 278 AA; 29778 WW; F894F955DDCD948A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                   57.1%; Score 140.5; D
22.5%; Pred. No. 0.3;
tive 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AA.
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01-DEC-2001 (TIEMBLREL 19, Last seq
01-DEC-2001 (TIEMBLREL 19, Last ann
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Matches 18; Conserv
                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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0924R8;
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069917; BAB63933.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0924P8 PRELIMINARY; PRT; 140 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
V23-D-J-C MU PROTEIN (FRAGMENT).
V23-D-J-C MU PROTEIN (FRAGMENT).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;                                                                                                                                                                                                                                                                                                                                                                                                                          YWMQXXXXXXXXXXXXXXEIDPSDSYTNYNQKFKGXXXXXXXXXXXXXXXXXXXXXX
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                                       Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; A1225171; CA865236.1; -.
HSSP; P01789; IMCP.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Ffam; PF00047; 1g; 1.
SWART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                     13060 MW; D816AD0858A47E4C CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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117 AA;
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
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                       SEQUENCE FROM N.A.
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SEQUENCE
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Q921K1
ID Q921K1
AC Q921K1
DT 01-DEC
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ö Gaps ö Query Match 56.9%; Score 140; DB 11; Length 146; Best Local Similarity 21.5%; Pred. No. 0.087; Matches 17; Conservative 51; Mismatches 11; Indels ( 16216 MW; 92460F1FDF1B7538 CRC64; 092407 PRELIMINARY; PRT; 145 AA. 092407; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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                                                                                                                                                                                                                  STRAIN=C57BL/6;

Rozono Y., Kozono H., Azuma T.;

Rozono Y., Kozono H., Azuma T.;

Rozono Y., Kozono H., Azuma T.;

Affinity Maturation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to PEMBL/GenBank/DDBJ databases.

EMBL; AB067793; BAB63278.1;
                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 145;
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2001 (TrEMBLrel. 19, Last annotation update)
ANII-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                          145 145
145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.7%; Score 139.5; DB 22.8%; Pred. No. 0.094; Live 49; Mismatches 1
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Matches 18; Conserv
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                                                                                                                                  NCBI_TaxID=10090;
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Kozono Y., Kozono H., Azuma T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069915;
NON_TER
                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%; Score 135.5; DB 11; Length 143; 21.5%; Pred. No. 0.19;
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143 AA; 15704 MW; C99D2433F2BADBAO CRC64;
                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
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V165-D-J-C MU.
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## ALIGNMENTS

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	X E	the second second	the state of the s
	X	Humanised and	Humanised anti-ras designed neavy chain ned i protein.
-	KW	Fas; antibody;	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
	ΚW	anti-allergic;	anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
	ΚW	dermatological	dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fa
	ΚW	nephrotropic;	nephrotropic; antiinfertility; neuroprotective; antlarteriosclerotic;
	Κ¥	hepatotropic;	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
_	ΚW	Hashimoto dise	ase; rheumatoid arthritis; graft versus host disease;
	KW	Sjorgen's synd	Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
	ΚW	Goodpasture sy	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
	ΚW	multiple scler	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
	ΚM	insulin depend	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
	ΚW	cardiomyopathy	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
	XX		
	OS	Synthetic.	
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	PN	EP990663-A2.	
	XX		
	PD	05-APR-2000.	
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	PF	29-SEP-1999;	99EP-0307711.
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<u></u>	PR	30-SEP-1998;	98JP-0276881.
	PR	30-SEP-1998;	98JP-0276882.
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_	PA	(SANY ) SANKYO CO LTD	OCOLID.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

110... 1111... 112... 114... 118... 118... 118... 118... 118...

Database

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SUMMARIES

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Humanised anti-Fas

AAW90933 AAW90934 AAW83037 AAB14779 AAW90929

AAW83036 AAB14776 AAW90926 AAW90936 AAM52156

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Description

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This invention describes a novel numanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capprosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, antiarterioscierotic, cardiant and hepatropic activity. (I) induce antiarterioscierotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive antiarterioscierotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive (disease associated with the Fas/Fas ligand system, especially systemic disease associated with the Fas/Fas ligand system, captions. (I) safety are synthemia gravis.

C disease, sociated with the Fas/Fas ligand system, con hypoplastic or anemia, Addison's disease, relemancial arthritis, graft oversus host disease, soleroderma, Goodpasture syndrome. Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively cells. They bind to both human and murine fass so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic cells. They bind to both human and murine fass so can be evaluated in inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I which is described in the method of the invention. infilammatory or autoimmune disease, induces apoptosis selectively in This invention describes a novel humanized anti-Fas antibody-like Tamaki I, Takahashi T; cells with abnormal Fas-Fas ligand systems Claim 2; Page 169-170; 263pp; English. Nakahara K, Haruyama H, WPI; 2000-258930/23. N-PSDB; AAA11644 

470 AA; Sequence

ö WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240 420 61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 Gaps 9 1 mgwsciilflvatatgvhsqvqlvqsgaevkkpgasvkvsckasgytftsywmqwvkqap 60 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS ö 100.0%; Score 2517; DB 21; Length 470; 100.0%; Pred. No. 5.3e-143; Live 0; Mismatches 0; Indels 0; Query Match 100. Best Local Similarity 100. Matches 470; Conservative 61 121 181 181 301 301 361 g à 셤 ò qq δ a ŏ g à g à

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosupressive; thyronimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; 361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420 insulin dependent diabetes mellitus; arterioscierosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection Takahashi T; 421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470 Humanised anti-Fas designed heavy chain Heu 2 protein. Serizawa N, Haruyama H, Nakahara K, Tamaki I, Ą. AAW90934 standard; Protein; 470 98JP-0276881. 98JP-0276882. 99EP-0307711. (first entry) (SANY ) SANKYO CO LTD. 08-AUG-2000 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; EP990663-A2. 05-APR-2000. Synthetic. AAW90934; N AAW90934 셤 õ

treating or preventing e.g. apoptosis selectively in New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems

2000-258930/23. N-PSDB; AAA11645 Claim 2 ; Page 174-176; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
CF and its ligand. The products of the invention have anti-inflammatory,
anti-anemnic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunoamodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antirheumatic, nephrotropic, antiinfertility, neuroprotective
antirheumatic, nephrotropic, antiinfertility, neuroprotective
antirheumatic, nephrotropic, antiinfertility, neuroprotective
antirheumatic, hephrotropic, antiinfertility, neuroprotective
antiphotision of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addisease, Siorgen's syndrome, speciality, mysathenta gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent dabetes mellitus, allergy, arterioscilerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatlatis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively

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Location/Qualifiers

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inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.
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                                                                                                                                                                   Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombopenia purpura; insulin-dependent diabetes; allergy; actory; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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                                                                                                                                                              99.9%; Score 2515; DB 21;
99.8%; Pred. No. 7e-143;
ive 1; Mismatches 0;
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                                                                                                                                                                               Best Local Similarity 99.8
Matches 469; Conservative
                                                                                                                      470 AA;
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This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFB7A. It includes humanising R4G and A76T amino acid substitutions that are includes humanising R4G and A76T amino acid substitutions that are are conserved in the human igG heavy chain. Host Escherichia coli pyHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion fragment of the humanised HV type HFB7A heavy chain and DNA croducing human igGl constant region (see AAV70080), and is deposited as FERM BP-6273 (Claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFB7A (see AAW83031-37), like native HFB7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antibodies are used to evaluate, in onimal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, graft versus host disease, solutoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allengies, atopy, arteriosclerosis, multiple scl rosis, Basedow's disease, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic myocarditis, cardiomyopathy, glomerular rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 225-227; 292pp; English.
                                             20..470
/label- Mat_protein
20..140
/label- Variable
                               /label- Sig_peptide
                                                                                                                141..464
/label- Constant
                                                                                                                                                                              /note= "claim 9"
69..84
                                                                                                                                                                                                                                    "claim 9"
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118..129
/label= CDR_H3
                                                                                                                                                 50..54
/label= CDR_H1
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97JP-0082953.
97JP-0169088.
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25-JUN-1997;
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Peptide
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Length 470;

Score 2514; DB 19; Pred. No. 8.1e-143;

99.98;

Query Match Best Local Similarity

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08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                       murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonophritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
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                       Gaps
                MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                                                                                                                   WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                               Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 Indels
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Mismatches
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N-PSDB; AAA72184.
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
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Pred. No. 8.1e-143;
1; Mismatches 0;
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ilarity 99.8%;
Conservative
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241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

241

301

WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

420 420

470

421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470 

AAW90935 standard; Protein; 470 AA.

AAW90935 RESULT

AAW90935;

361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV

YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS

360

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This introductor describes a novel numnized anti-ras antibody like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an order of the invention have anti-inflammetory, antidabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antidabetic, antidiffertility, neuroprotective, antiarteriosolerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit to prevent apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent chibibition of ligand binding. (1) are used to treat and/or prevent aboptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, relember, pernicious or hypoplastic anemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes menlitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, insulin dependent diabetes menlitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine anti-murine anti-pody HEPA designed heavy chain which is used in the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
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Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulomephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                              Takahashi T;
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                                                                                                                                                                                                                                                                                                                                                                                              Tamaki I,
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Pred. No. 8.1e-143
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.9%;
99.8%;
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                                                                                                                                                                                                                                         39-SEP-1999;
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                                                                                                                                                                                                                                                                                 30-SEP-1998;
                                                                                                                                                                                              05-APR-2000.
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                                                                                                            Synthetic
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Godpasture syndrome; crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
                                                                                                                            Fas; antibody; human; anti-inflammatory; anti-anemic; antidlabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi T;
                                                                                         Humanised anti-Fas designed heavy chain Heu 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 180-182; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0307711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0276881.
98JP-0276882.
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serizawa N, Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANY ) SANKYO CO LTD.
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                                                      08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                          EP990663-A2
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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continuous in cells with a normal system, by inhibiting binding between fas and its ligand. The products of the invention have anti-inflammatory, antidiabelic, anti-arthritic, antidization, contidiabelic, anti-allergic, anti-arthritic, antidization, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirioratic cardiant and hepatropic activity. (I) induce antiarteriosclerofic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent consenses associated with the Fas/Fas ligand system, especially systemic liques erythematosus, Hashimoto disease, rheumatoid arthritis, graft oversus host disease, Soloroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, anemia, Addison's disease, thrombopenia purpura, insulin calcingmopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively collinging apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minc inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
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470 AA; Sequence

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                                                                                                                                                          61 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrsedtavyycarnrd 120
                                                                                                                                                                                             WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                        YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                              GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                             YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                           241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                            KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                         Gaps
                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
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99.9%; Score 2514; DB 21; Length 470; 99.8%; Pred. No. 8.1e-143;
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                        1; Mismatches
                        469; Conservative
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Anti-Fas humanised antibody HFE7A heavy chain.

apptosis; HEFA, autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; sjogran syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthiritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopis arteriosclerosis; myocarditis; cardiomyopathy; cransplant rejection; therapy. humanised antibody HFE7A; monoclonal antibody; mouse; Fas;

Homo sapiens. Synthetic.

20..470 /label- Mat_protein /label= Sig_peptide Location/Qualifiers Peptide Protein

/label= Variable /label= Constant 50..54 /label= CDR_H1 464 20..140 Region Region Region

/note= "claim 9" /label- CDR_H2 /note= "claim 9" Region

/label- CDR_H3 /note- "claim 9" 118..129 Region

AU9859701-A.

08-0CT-1998

98AU-0059701 30-MAR-1998;

97JP-0276064. 97JP-0082953 97JP-0169088 08-OCT-1997; 25-JUN-1997; 01-APR-1997

(SANY ) SANKYO CO LTD.

un O, Kimihisa I; Tohru T; Jun 0, S, Shin Y, Hiroko Y, Nobufusa Hidevuki H, Masahiko O, Akio S.

WPI; 1998-543440/47.

N-PSDB; AAV70079

used to evaluate drugs in animal models and to treat Fas-associated allergy, atopy, arteriosclerosis, New antibodies and proteins bind conserved epitope of Fas antigen diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS

Claim 22; Page 212-213; 292pp; English.

This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. colipgHSL7A62 SANK 73397 harbors plasmid gpHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human igGl constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to 

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AAW83036 standard; Protein; 470

AAW83036 RESULT

(first entry)

15-MAR-1999

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AAW83036;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                              treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, sjoren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allerqies, atopy, arteriosclerosis, mnyocarditis, cardiomyopathy, qlomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                 121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                          MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                  241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                           301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                         Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                           Indels
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                                                                                                                                     99.4%; Score 2501; DB 19;
99.4%; Pred. No. 4.8e-142;
iive 1; Mismatches 2;
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                                                                                                                                                          Conservative
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                                                                                                                                                Similarity
                                                                                                       470 AA
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                                                                                                                                                          467;
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Best Local S:
Matches 467,
                                                                                                         Sequence
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the tracement or prevention of conditions such as autoimmune diseases, allery, acopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                                                   for the diseases caused by an abnormality
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                                                                                                                                                                                                                              in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
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l; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                     Claim 21; Page 95-96; 139pp; Japanese.
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                                                                                                                                                                                                         Preventive or treating agent
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98JP-0276883.
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                                                         (SANY ) SANKYO CO LTD
                                                                                                               WPI; 2000-485645/43.
N-PSDB; AAA72159.
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Matches 467; Conserv
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30-SEP-1998;
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AAW90926 standard; Protein; 470 AA
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08-AUG-2000

(first entry)

Humanised HFE7A designed heavy chain protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; antialpergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotroptc; antiinfertility; neuroprotective; antiarteriosclerottc; heparctropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardlomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2

05-APR-2000.

99EP-0307711 9-SEP-1999; 98JP-0276881 30-SEP-1998;

98JP-0276882 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Takahashi T; Nakahara K, Tamaki I, Serizawa N, Haruyama H,

2000-258930/23. N-PSDB; AAA11597

New humanized anti-Fas antibody, useful for treating or preventing e.g. cells with abnormal Fas-Fas ligand systems

Example reference 15; Page 134-136; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

co apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

contianemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosupressive thyromimetic,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

contianterioscleroric, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

antinhibition of ligand binding. (I) are used to treat and/or prevent

confiseases associated with the Fas/Fas ligand system, especially systemic

confiseases associated with the Fas/Fas ligand system, especially systemic

confiseases associated with the Fas/Fas ligand system, competitics, or serial and arthritis, graft

versus host disease, Sjorgem's syndrome, pernicious or hypoplastic

consultable sclerosis, Basedow's disease, thrombopenia purpura, insulin

consultable sclerosis, Basedow's disease, thrombopenia purpura, insulin

consultable mellitus, allergy, arteriosclerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively

colls. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models. (I) act on the active site of Fas, i.e. they mimic

the native ligand, do not induce liver disease, and have reduced risk of

the mathod described in the i

470 AA; Seguence

(SANY ) SANKYO CO LTD.

30-SEP-1998;

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                                                                                                                        GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                        360
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   Length 470;
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised HFE7A designed heavy chain HHH type protein.
Score 2501; DB 21;
Pred. No. 4.8e-142;
1; Mismatches 2;
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 99.48;
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98JP-0276882.
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                                Conservative
                 Similarity
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                Best Local Simi
Matches 467;
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   Query Match
Best Local 3
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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

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Into Introductor describes a nover numerized anti-ras antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an abnormal Fas/Fas apoptosis in cells with an operation building binding between geoperasis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomoulpressive, thyronimetic, antidiabetic, antidifertility, neuroprotective, antiarconforced, and antiarconforced, a
                                                                                                                                                                         New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like
                                  Ë
                                  Takahashi
                                  Tamaki I,
                                                                                                                                                                                                                                           cells with abnormal Fas-Fas ligand systems
                                  Nakahara K,
                                                                                                                                                                                                                                                                                                    Claim 2; Page 188-189; 263pp; English
                                  Haruyama H,
                                                                                        WPI; 2000-258930/23.
                                                                                                                       N-PSDB; AAA11655
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                                  Serizawa
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ö 240 240 300 360 121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 Gaps 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS ó; Indels DB 21; Score 2495; DB 21; Pred. No. 1.1e-141; 4; Mismatches 99.18; 98.78; Best Local Similarity 98.7 Matches 464; Conservative Query Match 121 181 181 241 301 301 361 g Q ŏ g g

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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytoctoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                    Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity folymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
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Pred. No. 1.4e-132;
3; Mismatches 10;
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                                                                                           AAM52156 standard; Protein; 731
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02-OCT-2000; 2000US-237159P.
                                                                                                                                                  (first entry)
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                                                                                                                                                05-FEB-2002
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                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                  Young RJ;
                                                                                                                       AAM52156;
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Matches
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MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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02-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                            polymorphic epithelial mucin; PEM1;
I; human; cytostatic; cancer; apoptosis.
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                                                      297
                                                                           301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                                             KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                          KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity foolymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                    LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                               Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
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                                                                                                                                                                                                                                                    Protein; 741
                                                                                                                                                                                                                                                                                                                                            Humanised monoclonal antibody; cytotoxic; endonuclease; DNase
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02-OCT-2000; 2000US-237159P.
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                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ANTI-) ANTISOMA RES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endonucleolytic activity
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                                                                                                                                                                                                                                                   AAM52159 standard;
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Gaps

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Indels

Length 741;

22;

93.2%; Score 2346.5; DB 22 93.0%; Pred. No. 1.4e-132; ive 20; Mismatches 10;

Query Match 93.2 Best Local Similarity 93.0 Matches 437; Conservative

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Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                      61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                237
           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody,
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                     YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                        358 kakgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppv
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                                                                                                                                                                                                                                                                                                                                         Novel compound used to treat cancer has target cell-specific pose comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                                                                                                                                                                                                                                   421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
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2000US-237159P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endonucleolytic activity
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Homo sapiens
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   Young RJ;
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                                                                                                                                                              Sequence
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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis
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                                                                                                                                             GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                           DB 22;
                                                                           Score 2341.5; DB 2
Pred. No. 2.7e-132;
                                                                                            20; Mismatches
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93.0%;
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2000US-237159P.
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specificity
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                                                                                    Local Similarity
                                                  729 AA;
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                                                                              comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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                                                         compound used to treat cancer has target cell-specific
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WPI; 2001-662969/76
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Best Local Similarity
Matches 436; Conserv
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                                                                                          03-APR-2000; 2000GB-0008049
02-OCT-2000; 2000US-237159P
                                                                    26-MAR-2001; 2001WO-GB01324
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                    WO200174905-A1.
                                             11-0CT-2001
Synthetic.
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Search completed: August 14, 2002, 15:15:37 Job time: 835 sec

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Appl Appli 
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STATE: Ca
COUNTRY:
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138.514 Million cell updates/sec
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Sequence 10, Appl
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                                                                                                              August 14, 2002, 15:17:04; Search time 82.88 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-049-672A-8
US-09-02-449-71
US-09-485-737B-67
US-09-485-737B-90
US-09-485-737B-90
US-09-437-642B-22
PCT-US93-07832-22
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US-08-887-352B-14
US-08-887-352B-16
US-08-466-151-65
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                                                                                                                                                                                                                                                                                              231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES:
CORRESPONDEME ADDRESS:
ADDRESSEE: William M. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                   ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                            ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 03-MAX-1993
ATTORNEY AGENT INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-326-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.1
Matches 420; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-458-516-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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2, A 18,

Sequence

US-09-109-207C-14 US-09-109-207C-16

US-08-887-352B-18

US-09-296-005-14 US-09-296-005-16 US-08-487-550-8

Sequence Sequence Sequence

8, A 45,

07-916-098A-45

.08-466-163B-8

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us-09-499-662-143.rai

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                                                                                                                                            119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
                                                              NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
                                                                              140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                         SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 259
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                                                                                                                                                                                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWWQWVKQAPGQGLEWMGEIDPSDSYTNY
                     260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                  320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC COMPATISHS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: S55 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                           440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUBBR: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTARTION NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6011
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08378939 Patent No. 5876961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DENGTH: 476 amino acids
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TOPOLOGY: linear
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: U.S.
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US-08-378-939-10
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61 GQGLEWMGGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDRY 120
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                                                                                                                                                                                                                                                                                        121 RQANFDRARVGWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVKFNWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAP 354
                                                                                                        Gaps
                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
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9
                                                                    Length 476;
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                                                                                                          Indels
                                                                                     Pred. No. 4.3e-158;
                                                                      DB 2;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                  88.6%; Score 2230; D
88.4%; Pred. No. 4.3e
Live 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Octley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN IMMEN OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                          Matches 421; Conservative
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 protein
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MEDIUM TYPE: Diskett
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                                                                      Query Match
Best Local Similarity
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MOLECULE TYPE:
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US-09-049-672A-8
             US-08-378-939-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                      235
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     SOFTWARE: WinPatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
                                                                                                                                                                                CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
   South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      650/952-9881
                                                 ZIP: 94080
COMEUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
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                                              94080
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US-09-026-985-71
                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
                                                                                                                                                                                                                                                                                                                                                                                                    7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: All Dony, Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                         Length 467;
                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                                                                                                                                                                                                                                                                                       87.5%; Score 2202.5; DB 4;
89.2%; Pred. No. 4.6e-156;
ive 19; Mismatches 28;
                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Genentech, Inc.
1 DNA Way
                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.29
Matches 414; Conservative
                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
STREET: 1 DNA WAY
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; CLONE: 2747531
US-09-049-672A-8
APPLICATION NUMBER:
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                FILING DATE:
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                                                                                                                                       TELEX:
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80 NQKFKGKATLIVDISISIAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVTV 138 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198 Gaps 9 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS Length 452; 17; Indels DB 3; Pred. No. 6.2e-156; 87.4%; Score 2200.5; 90.0%; Pred. No. 6.2e live 27; Mismatches

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421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Pate
SEQ ID NO 67
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                  APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.4%; Score 2200.5; DB 4; 90.0%; Pred. No. 6.2e-156; 1ive 27; Mismatches 17;
                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy of COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin //Genetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                           MBER: US/09/026,985
20-Feb-1998
Sequence 71, Application US/09026985 Patent No. 6133426 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,
                                           Gonzalez, Tania R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                        APPLICANT: Leong, Steven R.
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.08
Matches 407; Conservative
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TELEFAX: 6
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Best Local 3
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APPLICANT: BUYSE, MATIE-Ange
APPLICANT: BUYSE, MATIE-Ange
APPLICANT: BUYSE, MATIE-Ange
APPLICANT: BUYSE, MATIE-ANGE
APPLICANT: SABLON, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC.SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 1998-06-14
PRIOR APPLICATION NUMBER: EPO 9870139.7
PRIOR FILING DATE: 1998-06-18
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US-09-485-737B-67; Sequence 67, Application US/09485737B; Patent No. 6350860
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US-09-485-737B-90
; Sequence 90, Application US/09485737B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: SYNTHETIC
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E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            CURRENT APPLICATION DAMP:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                  WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee, wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO7
TELECOMMUNICATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
                                                                                                                                                                                    SOFTWARE:
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                                                   STATE: Ca
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       GENERAL INFORMATION:

APPLICANT: BUYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
TITLE OF INVENTION: INTERPERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS.015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT PILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PAPLICATION NUMBER: EPO 98870139.7
PRIOR PAPLICATION NUMBER: EPO 97870122.5
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 90
LENGTH: 711

MANDER OF SEQ ID NO 90
LENGTH: 711

MANDER OF SEQ ID NO 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 THICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 WMGEIDPSDSYTNYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 LISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.5%; Score 2177; DB 4; Length 711;
88.2%; Pred. No. 6.3e-154;
Live 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
PAPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: SYNTHETIC US-09-485-737B-90
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Matches 410; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                     80 NQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
                                                                                                                                                       LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                                                                                                                                                 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256
                                   Gaps
                                                                  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                       1 QVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSH
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                                 3;
                                   Indels
 DB 2;
                                28;
; Score 2161.5; DB 2,
; Pred. No. 4.9e-153;
17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Query Match 85.9%;
Best Local Similarity 89.4%;
                                 Matches 406; Conservative
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80 NOKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
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                                                         SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.9%; Score 2161.5; DB 5; Best Local Similarity 89.4%; Pred. No. 4.9e-153; Matches 406; Conservative 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              Sequence 22, Application PC/TUS9307832
Sequence 22, Application PC/TUS9307832
GENERAL INFORMATION:
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                  437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                       421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUBBRE: 07/715272
FILING DATE: 14-JUN 1991
PRIOR APPLICATION DATA: PCT/US92/05126
APPLICATION NUBBRE: PCT/US92/05126
FILING DATE: 15-JUN 1992
PRIOR APPLICATION DATA:
FILING APPLICATION NUBBRE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Genericch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19930820
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REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 454 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMFUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA:
                                Sequence 22, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.9%; Score 2.0.
89.4%; Pred. No. 4.9e.
+ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 15-JUN-1992
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 454 amino acids TYPE: Amino Acid
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Matches 406; Conservative
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US-08-437-642B-22
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                  US-08-437-642B-22
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256
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                                                                                             LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: EDELANN, LENA
APPLICANT: EDELANN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABHII, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHMAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/793,450 FILING DATE: 03-MAR-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILLING DATE: 0.2-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                     437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pale
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08793450 Patent No. 6312690 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Sequence 14, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-TgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                      120 Y--KWKYHGDWFDPWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 177
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                                                  Gaps
                                                                                                                        298 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPI
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                                               8;
Length 472;
85.2%; Score 2144; DB 4; Length 4
84.8%; Pred. No. 1e-151;
ive 27; Mismatches 37; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-JU-1997
CLASSIFICATION: 530
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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TELEPHONE: 650/225-1489
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
Query Match
Best Local Similarity 84.88
Matches 403; Conservative
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INFORMATION FOR SEQ ID NO:
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US-08-887-352B-14
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FELECOMMUNICATION INFORMATION:
              TELEPHONE: 650/225-148:
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAM Way
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                                                                                                                                                                                                                                                                                      SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                   259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                       Length 451
                                                                                                         3 2124;
. No. 3e-150;
. ___hoq 30; Indels
                                                                                                      84.4%; Score 2124; DB 2;
87.6%; Pred. No. 3e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 03-01-1997
                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/088873528 Patent No. 5994511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SVODGGA, Craig G,
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: South San Francisco
STATE: California
COUNTRY: USA
              : 451 amino acids
Amino Acid
                                                                                                                                    Conservative
SEQUENCE CHARACTERISTICS
                                            Linear
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                          ; TOPOLOGY:
US-08-887-352B-14
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                                                                                                                     Best Local Sim
Matches 396;
                                                                                                       Query Match
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79 YNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
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                                                                                                                                                                                                                      SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
                                                                                                                     Length 451;
                                                                                                                   84.4%; Score 2124; DB 2;
87.6%; Pred. No. 3e-150;
tive 24; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/08466151 Patent No. 6037453 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                      Best Local Similarity 87.69
Matches 396; Conservative
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SOFTWARE: WinPatin (G
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
                                   ; TOPOLOGY: Linear
US-08-887-3528-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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Thu Aug 15

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; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-14
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1990-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
                                                                                                                   TYPE: PRT ORGANISM: Artificial
                                                                                                                                              FEATURE: NAME/KEY: Artificial
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Job time: 688 sec
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Best Local S
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Improved Anti-1gE Antibodies and Method of Improving Polypeptide
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87.6%; Pred. No. 3e-150;
tive 24; Mismatches 3
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PRIOR APPLICATION NUMBER: 08/466150.
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
APPLICATION NUMBER: 08/185899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-109-207C-14

Sequence 14, Application US/09109207C
Patent No. 617213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
TITLE OF INVENTION: Improved Anti-Ig
                                                                                                                           APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                     APPLICATION NUMBER: 07/744768 FILING DATE: 14-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                INFORMATION FOR SECTIONO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.6
Matches 396; Conservative
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                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              Amino Acid
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US-08-466-151-65
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SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 YNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
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                                                                    Gaps
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84.4%; Score 2124; DB 4; Length 4:
87.6%; Pred. No. 3e-150;
... ...matches 30; Indels
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                                                                  Matches 396; Conservative
                                             Similarity
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

August 14, 2002, 15:18:59 ; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

US-09-499-662-143
2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Id damma-1 chain C		gamma-3	gamma-2a	~		gamma-2				g gamma	Ig heavy chain V r	c	Ig gamma 2a chain			qamma chain C	gamma 1 chain	gamma chain C				gamma-3 heavy	gamma-1 chain		gamma-1 chain		chain	
ID	СКНО	A23511	A60764	537483	G2HU	G4HU	G2MS11	S40295	S01321	\$22080	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	G1MS	PS0018	GIMSM	G3MSM
DB	-	~	7	7	Н	Н	Н	7	7	~	7	N	7	~	7	4	~	~	-	7	-	7	Н	N	Н		7	П	Т
Length DB	330	377	377	469	326	327	474	446	475	470	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
% Query Match	69.8	65.1	65.1	64.1	64.0	63.5	61.5	61.5	59.8	58.6	58.3	56.9	56.7	50.3	50.1		49.5		48.9	48.9	48.1	46.3	46.0	45.9	45.7	٠	45.5	45.3	45.3
Score	1758	1639.5	1637.5	1613.5	1610	1599.5	1549	1547	1504.5	1474	1467	1432	1426.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
Result No.	,	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	G2MSBM	147162	S38864	S14683	S04845	S69131	838950	A49444	S69340	B46529
Н	N	<del>, ,</del>	Н	7	7	Н	~	7	7	~	~	7	7	~	~
330	329	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.6	37.5	36.8	34.5	33.9	31.7	30.3	30.2
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	966	943	925.5	867.5	854	798	762.5	759.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1	
Iq qamma-1 chain C region - human	
C; Species: Homo sapiens (man)	1000 t = 1.11 = 21 - 000 t = 1.11
C;Date: 31-Jan-1981 #Sequence_revision 18 Aug-1982 #text_cnange 10-Jul-1999 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146	t_cnange 16-Ju1-1999 1668; A91723; A02146
R; Ellison, J.W.; Berson, B.J.; Hood, L.E.	
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal	ılin C-gammal gene.
A; Reference number: A93433; MUID:82274238	
A; Accession: Ay3433	
A; Molecule cype: DNA A: Residues: 1-330 <fil></fil>	
A;Cross-references: EMBL:217370	
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker	97-Lys, and the Glm(1) marker
A;Note: Lys-330 is removed after translation	
submitted to the EMBL Data Library, October 1992	
A; Reference number: S33904	
A;Accession: S36861	
A; Molecule type: DNA	
A; Residues: 2-330 <har></har>	
A; Cross-references: EMBL: 217370	;
RiTakahashi, N.; Veda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.	ıı, S.; Konjo, T.
0(11.24) b/1-0/5/ 1982 A. Hittle: Ctturchure of bumen immunocalchulin remme genee, implications for suclution of	implications for evolution of
A:Reference number: S33887. MITD:83001943	the control of control of
A: Accession: S33887	
A; Molecule type: DNA	
A; Residues: 88-113; 235-330 <tak></tak>	
, U.; Gall,	W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970	
A;Title: The covalent structure of a numan gammaG-immunoglob	gammag-ımmunoglobulin, VII. Amino acıd seq
A: Contents: mvelone protein Bu	
A: Accession: B90563	
A; Molecule type: protein	
A; Residues: 1-96, 'R', 98-135 <cun></cun>	
A; Note: this sequence has the Glm(3) marker, 97-Arg	
R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.	sberg, W.H.; Edelman, G.M.
Blochemistry 9, 31/1-3181, 19/0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
A) TILLE: THE COVALENT STRUCTURE OF A DUMBAN GAMMAGG-IMMUNOGIODULIN. VIII. AMINO ACID	logiobulin. Viii. Amino acid se
A. Kelefence unmber: Asussa, Mulb:/luoauzs	
A; contents: Eu A; Accession: A90564	
A; Molecule type: protein	
A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2	,'N',196-197,'D',199-238,'E',2
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met	ilu and 241-Met
Rybons Lingt, h.; hillschindin, N.	
noppersoyiel S L Filystor. Chem. 337, 1371—1004, 1370 noppersoyiel S L Filystor. Chem. 237, 1371—1004, 1370 northing Drimsoretruktur cince monotlopalar 1231—1000 (Mucalomaratein Ni	minglobiling / Mwolomorotoin Ni
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c5, u) with an IGHG4 conv
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A; Residues: 1-377 <HUC>
A; Cross-references: GB:X03604; GB:M1295B; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics: GBB:IGHG3
A; Genes: GBB:IGHG3
A; Genes: GBB:IGHG3
A; Genes: GBB:IGHG3
A; GBB:IGHG3
                                                                                                                                                                                                                                                        R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                         Tig gamma-3 chain C region (allotype G3m(b)) · human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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C;Date: 14 May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an A;Reference number: A60764; MUID:90007613
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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|ALHNRFTQKSLSLSPGK 377
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Matches 312; Conservative
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A. Residues: 1-96, "K', 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 <SCE
A. Mote: this sequence has the Glm(3) and Glm(non-1) markers
A. Mote: this sequence has the Glm(3) and Glm(non-1) markers
B.Gall, W.E.; Edelman, G.M.
Blochemistry 9, 3188-3196, 1970
Blochemistry 9, 3188-3196, 1970
A. Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A. Reference number: A00565; MUID: 71064027
A. Contents: annotation; disulfide bonds
A. Foreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Seichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. The primary structure of monoclonal IgG1 immunoglob
A. Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A. Reference number: A91667; MUID: 77070267
A. Contents: annotation; disulfide bonds
C. Genetics:
                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Note: this sequence has the Gim(17) and Gim(1) markers
A; Note: this sequence has the Gim(17) and Gim(1) markers
B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOL
A; Reference number: A91723; MUID: 83289131
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
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A: Map position: 14q32.33-14q32.33
A: Map position: 14q41; 224/1
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IQA and IGM, the subunits associate into la C: Superfamily: immunoglobulin hemology immunoglobulin hemology cimic immunoglobulin homology cimic first and interchain (to heavy chain) #status experimental F: 103/Disulfide bonds: interchain (to heavy chain) #status experimental F: 109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
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Pred. No. 3.6e-93;
3; Mismatches 0;
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igen Primaerstruktur.
A; Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: 891668
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99.1%;
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Matches 327; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S3483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                             238
                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLKWIGWIYPASGNTKYNENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKFKDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                        Gaps
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                                                                                                                           Length 377;
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A. Accession: 837483
A. Status: preliminary
A. Holecule type: mRNA
A. Residues: 1-469 < DUC>
A. Residues: 1-469 < COUCA
A. Residues: 1 | 469 < COUCA
A. Residues: 1 | 469 < COUCA
A. Residues: I | 460 < COUCA
A. Residues: 
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                                                                                                                        Score 1637.5; DB 2;
Pred. No. 3e-86;
7; Mismatches 11;
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64.6%; Pred. No. 9e-85;
ive 59; Mismatches 10
                                      <IWW>
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology
                                                                                                                           65.1%;
82.8%;
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305; Conserv
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Matches 305;
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Best Local
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A; Molecule type: DNA
A; Residues: 1-36 < FLL.
A; Residues: 1-36 < FLL.
A; Cross.references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
A; Varuay A.C.; Tuung, E.; Pudennoberg, H.H.
J; Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, an A; Reference number: A92809; MUID:81007873
A; Contents: myeloma protein Til
A; Accession: A92809
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60-Ala and in the amid
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Note: Trp-156 is at or near the complement-binding site
A; Note: Trp-156 is at or near
A; Note: Trp-166 is at or near
A; Connell, G.E.; Parr, D.M.; Hoffmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; The amino acid sequences of the three heavy chain constant region domains of
A; Reference number: A90752; MUD: 80001357
A; Contents: myeloma protein Zie
A; Accession: A90752
A; Molecule type: protein
A; Residues: 1-24, E', 26-57, EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', A; Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2 chain C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
R;Ellison, J.; Hood, L.
A;Tile: Linkage and sequence homology of two human immunoglobulin gamma heavy of A;Reference number: A93906; MUID:82197621
A;Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 121, 217-225, 1971
A; Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A; Reference number: A90253; MUID:72033500
A; Contents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                             NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                     359 ISKAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                           A; Contents: Zie
A; Accession: A93132
A; Molecule type: protein
A; Residues: 238-275 < H0F>
R; Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, 8
A; Note: the revised sequence differs from that shown in having (
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MOL. Influndol. 16, 923-925, 1979
A.Title: A note on the amino acid sequence
A;Reference number: A93132; MUID:80114419
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A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14432.33
A;Map position: 14432.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c;Complex: An immunoglobulin heterotetramer subunit sasociate into C;Superfamily: immunoglobulin c region; immunoglobulin homology
C;Superfamily: immunoglobulin c region; immunoglobulin homology cimi>F;20-85/Domain: immunoglobulin homology cimi>F;39-10/Region: hinge
F;39-10/Region: hinge
F;34-203/Domain: immunoglobulin homology cimi>F;240-307/Domain: immunoglobulin homology cimi>F;240-307/Domain: immunoglobulin homology cimi>F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83.141-201, 247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;17/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity
Matches 303; Conserv
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A;Gross-references: GDB:119338; OMIM:147110
A;Map position: 14932.33-14932.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kind bain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85,Domain: immunoglobulin homology <IM2>
F;20-85,Domain: immunoglobulin homology <IM2>
F;14,Opmain: immunoglobulin homology <IM2>
F;14,Domain: immunoglobulin homology <IM3>
F;14,Disulfide bonds: interchain (to light chain) #status experimental
F;102.103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107,Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Sate: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C.Sacession: 490933; Asology, And 150
R.Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A.; Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A; Reference number: A90933; MUID:83157104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-37 < ELL>
A; Note: the sequence was determined from the germline gene
A; Pote: the sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
A; Title: Human immunoglobulin sublclasses. Partial amino acid s
A; Reference number: A90249; MUID: 70207560
A; Molecule type: protein
A; Residues: 1-30; 81-326 < PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 64.0%; Score 1610; DB 1; al Similarity 91.8%; Pred. No. 9.4e-85; 303; Conservative 10; Mismatches 13;
                                  G.
                                  of immunoglobulin
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Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobuli
A;Reference number: A93157; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
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Matches 303; Conserv
                                                                                                                                              A; Gene: GDB: IGHG2
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A;Gene: GDB
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GDB: IGHG4

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usema-1b chain - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C; Accession: S25057; A02157; A26233; A2633; A53598
R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
R; Pescher on unmber: S25057
A; Reference number: S25057
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-474 <FIS>
A; Reference number: A02157; MUD:80120716
A; Accession: A02157
A; Accession: Acc
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    327;
    Length
                                                                                       Indels
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Blattner, F.R.
    1;
63.5%; Score 1599.5; DB 1;
illarity 91.8%; Pred. No. 3.7e-84;
Conservative 9; Mismatches 15;
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A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germl:
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blatti Science 206, 1299-1303, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date. 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Accession: S40295 # Sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Accession: S40295 # S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C. submitted to the EMBL Data Library, January 1993
A. Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 agas: A; Reference number: S40295
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-446 < KLED-
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C; Superfamily: immunoglobulin C region; immunoglobulin pyroglutamic acid
C; Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
C; Reywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F; 1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F; 118-446/Domain: C region <CHP>
F; 118-446/Domain: C region <CHP>
F; 118-446/Domain: C region <CHP>
F; 118-446/Domain: C2 region <CHP>
F; 231-340/Domain: C2 region <CHP>
F; 231-340/Domain: G2 region <CHP>
F; 231-340/Domain: G3 region <CHP>
F; 221-350/Fedion: immunoglobulin homology <IMM>
F; 1/Modified site: pyrrollidone carboxylic acid (Gln) #status predicted
F; 132-96, 144-199, 251-351, 367-452/pisulfide bonds: interchain (to light chain) #status predicted
F; 224, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 227, 229/Disulfide bonds: interchain #status predicted
F; 224, 227, 227, 229/Disulfide bonds: interchain #status predicted
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                                                                                                                             PIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENN 413
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                                                                                                                                                                                                                                                                                                         414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                       SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPEL
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64.6%; Pred. No. 5.1e-81;
tive 58; Mismatches 94;
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Best Local Similarity
Matches 292; Conserv
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                                              A ARREFERENCE NUMBER: A2535, MUID: 80081501
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untranslated regions of the murine gamma2b
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Matches 293; Conservative
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A; Reasidues: Preliminary
A; Molecule type: mRNA
A; Residues: L-70 < SAN>
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
B; Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g.
A; Reference number: S06610; MUID:90097956
A; Reference number: S06610; MUID:90097956
A; Residues: 142-470
A; Residues: 142-470
A; Residues: EMBL:X16701
A; Rote: the sequence was determined from the germline gene
C; Genetics:
A; Genetics: Immunoglobulin C region; immunoglobulin membrane protein
F; 161-225/pomath: immunoglobulin homology
C; Keywords: glycoproteten, heterotetramer; immunoglobulin, membrane protein
F; 161-225/pomath: immunoglobulin homology c; Newyords: glycoprotein heterotetramer; immunoglobulin homology
E; MB/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S31459
R;Patri, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.6%; Score 1474; DB 2; Best Local Similarity 60.2%; Pred. No. 7.8e-77; Matches 284; Conservative 63; Mismatches 115;
                            R;Sanders, P.G. submitted to the EMBL Data Library, November 1991 A;Reference number: $22080 A;Accession: $22080
C; Accession: $22080; $06610; A31303
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Cibate: 30-59p-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
Cibates: 30-59p-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
CiAccession: S01321
Ride Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. J. Bloochem. 176, 287-295, 1988
Bur. J. Bloochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Reference number: S01320; MUID:88329081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781 A:Note: this sequence was determined from the differentiated gene C:Superfamily: immunoglobulin C region; immunoglobulin C region; immunoglobulin C:Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                        SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma-2b chain precursor - mouse
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A; Molecule type: mRNA
A; Residues: 1-475 <DE1>
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Best Local Similarity
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C;Species: Homo sapiens (man)
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MuID:9526268?
A;Reference number: S69339; MuID:9526268?
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: I-374 < KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
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                                                                                                                                                                                                                                                                                                                                       SSHAFAYASYDFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYK 415
                                                                                                                                                                                                                                                                                                                                                                                     NNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLEWMGEIDPSDSYTNYNOKFKGKATLIVDTSTSTAYMELSSLRSEDTAYYYCARNRDYS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
                                                                                                                                                                                                                 Gaps
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A;Accession: $72664
A;Status: preliminary
A;Molecule trype: mRNA
A;Residues: 1-140, °C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                           homology
                                                                                                                                                                           Match 58.3%; Score 1467; DB 2; Length 4 Local Similarity 59.4%; Pred. No. 2e-76; les 282; Conservative 67; Mismatches 114; Indels
A; Accession: S31459
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-472 < PAID>
A; Cross-references: EMEL: X69797
C; Superfamily: immunoglobulin C region; immunoglobulin C; Reywords: immunoglobulin E; 277-346/Domain: immunoglobulin homology < IMM>
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Best Local S:
Matches 282,
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Saccession: PC4436
R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Haradi, Biochem: Biophys. Res. Commun. 240, 566-572, 1997
A; Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A; Reference number: JC5810; MUID:98063277
A; Reference number: JC444
A&AA>
C; Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against immunoglobulin homology
C; Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against immunoglobulin homology
F; 251-320/Domain: immunoglobulin homology **Status predicted*
F; 29/Disulfide bonds: interchain (to 98) **status predicted*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL 421
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                                                                                         Gaps
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    Length 374;
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Score 1432; DB 2;
Pred. No. 1.5e-74;
3; Mismatches 58;
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                                                                                     28;
56.98;
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57.8%;
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Search completed: August 14, 2002, 15:19:00 Job time: 688 sec
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21 Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;KacsKovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Fitle: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Fitle: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147159
A;Accession: 147159
A;Accession: 147159
A;Reference number: If Internal ated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <AAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: Immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                         254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
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Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;RacsKovics, I;Sun, J;Butler, J.E.
J. Immunol. 153, 356-3573, 1994
A;Title: Five puttative subclasses of swine IgG identified from the cDNA sequence number: 147158; MUID:95015845
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics:
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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;; Pred. No. 6.8e-65;
41; Mismatches 54;
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Best Local Similarity 69.6%;
Matches 231; Conservative 41
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 14, 2002, 15:23:13 ; Search time 53.64 Seconds (without alignments) 339.265 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-499-662-143
2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	homo	homo	homo		P01862 cavia porce			P22436 mus musculu	P01868 mus musculu	P20761 rattus norv	P01869 mus musculu	snw /	P01863 mus musculu	P20762 rattus norv	P01864 mus musculu	P01865 mus musculu	P20760 rattus norv	Enm	P01867 mus musculu	P01751 mus musculu	P01750 mus musculu	P01755 mus musculu	mus	P01749 mus musculu	P01746 mus musculu	P01753 mus musculu	P01748 mus musculu	P06328 mus musculu	P01855 rattus norv	P01854 homo sapien	P01754 mus musculu	1	P23083 homo sapien
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## ALIGNMENTS

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                                                                                                                                       Delsenhofer J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus auceus at 2.9- and 2.8-A resolution.";

Blochemistry 20:2361-2370(1981).

-I-MISCELLANGOUS: NE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-MISCELLANEOUS BU ALSO DIFFERS IN THE AMIDATION STATES OF SESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                                 Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L. and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                              268-272.
-I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
RESIDUES 198,2678272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ).
REMOVED POST-TRANSLATIONALLY.
K -> R (IN GIM(3) MARKER).
/FIId-VAR_003886.
D -> E (IN GIM(NON-1) MARKER).
/FIId-VAR_003887.
L -> M (IN GIM(NON-1) MARKER).
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed-7236608;
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HINGE.
CH2.
CH3.
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                             DISULFIDE BONDS.
MEDLINE-77070267; PubMed-1002129;
         lochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
 Intrachain disulfide bonds.";
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PDB; IFC1; 15-JUL-92;
PDB; IFC2; 15-JUL-92.
MIM; 147100;
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330
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Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1Ggamma-2 chain C region.
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Mammalia; Eutheria; Primates;
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Matches 327; Conservative
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GC4_HUMAN
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                                                                                                                                                                                                                          TISSUE-Fetal liver;
MEDLINE=8423592; PubMed=6329676;
Krawlinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamme heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
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                       SEQUENCE OF 2-326 FROM N.A.
MEDILIPE-81219(521; PubMed-6804948;
Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of human
                                                                                                                        TISSUE-Fetal liver;
MEDLINE-83001943; PubMed-6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo 'Structure of human immunoglobulin gamma genes: implications evolution of a gene family.";
Cell 29:671-679(1982)
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MEDLINE-80114419; PubMed=118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
                                                                          chain constant region genes.";
Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=69064124; PubMed=5782707; Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 25; 59; 60 AND 264-268 (ZIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
                                                                                                                                                                                                                                                                                                                                           MEDLINE-81007873; Pubmed-6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IqC
                                                                                                                                                                                                                99-177 AND 310-326 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95255298; PubMed=7737190;
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Mol. Immunol. 16:923-925(1979)
                                                                                                 [2]
SEQUENCE OF 88-115 FROM N.A.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S -> A (IN MYELOMA PROTEINS TIL & ZIE).
TYTIG-VAR-003889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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Pred. No. 1.5e-103;
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91.8%; Pred. No. 1.5e-
+ive 10; Mismatches
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(Rel. 01, Last sequence update)
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CH2.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
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178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                                                  GC_RABIT
P01870;
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVUSVLTVLHQDWLNGKEYKCKUSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVFLFFPKFFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-70207560; PubMed-4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the Constant region of a gama 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.W., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305
35940 MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                          SMART; SNO0410; ĬĠ_like; 1.
SMART; SNO0407; IĠG_l
SOSTIE; SSO0290; IĠ_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 1599.5; DE
91.8%; Pred. No. 8e-103;
 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             CH1.
HINGE.
                                                                                                                                                                                                                                                                                           EMBL; K01316; AAB59394.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                          SEQUENCE OF 1-30 AND 81-326.
         gamma-4 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                  P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                      DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                        A02150; G4HU
                                                                                                                                                                                                                                                                                                                HSSP; P01842;
MIM; 147130;
 16-0CT-2001
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DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-6135469; PubMed-1243651; Pratt D.M., Mole L.E.; Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma
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Ig gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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HILL R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.; (In) Killander J. (eds.); (In) Killander J. (eds.); Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-70110015; PubMed-5461106; Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.; Sequence studies of the Fd section of the heavy chain of rabbit imminodiobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 88-266 FROM N.A.
MEDLINE-81299977; Pubmed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of tabbit 1gG: isolation of a cDNA encoding is heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           323 AA
                                                                                                                                                QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                              298 QEGNVFSCSVMHEALHNHYTQKSLSLGK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84030930; PubMed-6313520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 18:387-397(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 151:337-349(1975).
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                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 132-161.
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HSSP; P01857; 1FC
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BIOChemistry 10:36-31(1971).

-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 UNBED GUINEA PIGS.

PIN 13 UNBED GUINEA PIGS.

HSSP; P01772; 2FB4.

InterPro; IPR00360; Ig_MC.

InterPro; IPR003697; Ig_C1.

InterPro; IPR003600; Ig_lke.

Pfam; PF00047; ig; 3.

SMART; SM00407; IG_l; 2.

PROSITE; PS00290; IG_MHC; 1.

RMANT; SM00407; IG_L; 2.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-71058474; PubMed=4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                          pig
the carboxyl-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH--TCPPCPAPEL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGLYSLTSMVTVPSSQKAT - - - CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPEN 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 227-311.

WEDLINE-7036073. PubMed-4609467;

Trischmann T.M., Cebra J.J.;

"Primary structure of the CH3 homology region from guinea pig 19G2
                                                                                                                                                                                                     MEDLINE-75036072; PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%; Score 1210.5; DB 1; Length 329; 69.8%; Pred. No. 3.9e-76; Live 30; Mismatches 62; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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105 INTERCHAIN (WITH A HEAVY CHAP)
110 INTERCHAIN (WITH A HEAVY CHAP)
1202 INTERCHAIN (WITH A HEAVY CHAP)
1308 N-LINKED (GLCNAC...).
178 N-LINKED (GLCNAC...).
                                                                                                    Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-(71). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
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                                                                               SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                      Biochemistry 13:4804-4811(1974).
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                                                                                                                                                                                          SEQUENCE OF 134-226.
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142
178
248
329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           GC2_CAVPO STANDARD; PRT; 329 AA.
P01862;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last cannotation update)
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                         Length 323;
                                                                                                                                                                                                                                                                                                                                                             57; Indels
                                                                           M (IN D11 MARKER).

A (IN E15 MARKER).

E (IN REF. 2).

E (IN REF. 3 AND 4).

E (IN REF. 5).

D (IN REF. 5).

C (IN REF. 5).

E (IN REF. 5).

D (IN REF. 5).

O (IN REF. 5).
                                                                                      1 -> A (IN D11 MARKER).
1 -> A (IN D11 MARKER).
1 -> E (IN REF. 2).
2 -> E (IN REF. 2).
3 -> E (IN REF. 5).
3 -> E (IN REF. 5).
3 -> E (IN REF. 5).
5 -> E (IN REF. 5).
5 -> C (IN REF. 5).
6 -> Q (IN REF. 5).
6 -> Q (IN REF. 5).
7 -> D (IN REF. 5).
8 -> D (IN REF. 5).
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                                                      domain; Immunoglobulin C region,
                                                                                                                                                                                                                                                                                                                                      48.9%; Score 1231.5; DB 70.0%; Pred. No. 1.4e-77 tive 34; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 4-68.
MEDLINE=71058471; PubMed=5538606;
                                                                                            HZ>OZOZOWZWZZXZ
                                                                                                                                                                                                                                                                                                35404 MW;
                                       PROSITE; PS00290; IG_MHC; 1.
IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                                      Query Match 48.9°
Best Local Similarity 70.0°
Matches 229; Conservative
         Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
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323 AA;
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VARIANT 104
VARIANT 185
CONFLICT 71
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GC2_CAVPO
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-1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CHI REGION.
-1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
GAMMA-3 HEAVY CHAINS.
-1- MISCELLANEOUS: DISEASE PROTEIN OWN MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
-1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                            435
318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
                                                                                                                   295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frangione B., Rosenwasser E., Prelli F., Franklin E.C.; "Prinary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Biochemistry 19:4304 4308 (1980).
                      378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).

MEDLINE-82247835; PubMed=6608505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene deletion model.";
Proc. Natl. Acad. Sci. U.S. A. 79:3260-3264(1982).
-!- SUBUNI: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human 1gG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Franklin E.C.; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoqlobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)
1GHG3.
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                                                                                                                                                       469
                                                                                                                                                                                                                                                                                             290 AA
                                                                                                                                                                            296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                       436 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
                                                                                                                                                                                                                                                                                             STANDARD;
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P01860;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                      domain; Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC N-LINKED (GLCNAC. . .).
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/FTId=VAR_003891.
F -> Y (IN OMM).
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T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
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F -> Y (IN OMM).
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Pred. No. 7e-73;
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46.2%; Score 1162; D
Best Local Similarity 91.4%; Pred. No. 7e-7
Matches 212; Conservative 11; Mismatches
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                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
PERM; PF00047; Ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00299; IG_MHC; 1.
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HSSP; P01857; 1FC1.
MIM; 147120; -
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179 ISKTKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
                                                                                                                                       Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                          Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | SEVSSVFIFPPRPKPUDVLITILIPRVICVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CHAIN).
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CHAIN).
                419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                         region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 326;
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(WITH A HEAVY C
(WITH A HEAVY C
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63.4%; Pred. No. 2.4e-72;
tive 52; Mismatches 60;
                                                                          GC1_RAT STANDARD; PRT; 326 AA. P20759; 01-FEB-1991 (Rel. 17, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 19 gamma-1 chain C region.
                                                                                                                                                                                                        Constitution of the fact immunicy tobulin gamma Gene 74.473.482(1988).

PIR; PS0017; PS0017.

HSSP; P01842; 7FRB.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_c1.

Pfam; PF00047; Igc; 3.

SMART; SMOM407; IGC]; 2.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region.

DOMAIN 1 97 CH1.
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CH2.
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MEDLINE-89232738; PubMed=3149946;
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Rattus norvegicus
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blather F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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Pred. No. 5.5e-72;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
19 gamma-3 chain C region, secreted form.
Mus musculus (Mouse)
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380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
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MEDLINE-80202559; PubMed=6769752;
MEDLINE-80202559; PubMed=6769752;
MEDLINE-80202559; PubMed=6769752;
Mano Y., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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                             Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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"Evolution of immunoglobulin subclasses. Primary structure murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE=80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an in
                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
II gamma-1 chain C region.
Mus musculus (Mouse).
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Nucleic Acids Res. 6:3305-3321(1979).
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MEDLINE-73008889; PubMed-5073237;
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
PIR; A02159; GIMS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
Pfam; PF00047; Ig 3.
SMART; SM00407; Ig 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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01-FUL-1999 (Rel. 38, Last annotation update)
1g gamma-2B chain C region.
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MEDLINE=89232738; Pubmed=3149946;
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324 AA;
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Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
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                                                                                                                                                                                                                                                                         201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS-----CDKTHTCPPCPA 254
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-80045035; MEDLINE-80045035; PubMed-115593; Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                         Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-AVG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
                                                                                         Immunoglobulin domain; ווmmunoglobulin C region.
NON_TER
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                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam. PF00047; Ig; 3
SMART; SM00410; IG_like; 1.
                                                                                       PS00290; IG_MHC; 1.
                                                                                                                                                                                                                        214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
               Gene 74:473-482(1988).
PIR; PS0018; PS0018.
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106
109
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333 AA;
                                HSSP; P01842; 7FAB.
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P01869;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-44 FROM N.A.

MEDLINE=8222190; PubMed=65283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                                  Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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                                                                                                                                                                                                                  SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; PubMed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl lessenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
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4CC88343B7A1CE27 CRC64;
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                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
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СН3.
SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; PubMed-6804950;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
Pfam; Pfam; SM00407; ig; 3.
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393 AA;
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                                                                                                       318
                                                                                                                173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 232
                                                      201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                    319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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        ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                   259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3;2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                     23-OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma -3 chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                  398 AA.
                                                                                                                                                                                                                                               439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
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                                                                                                                                                                                                                                                            EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_like.
Pfam; PF00047; ig; 3
SMART; SM00410; IG_like; 1.
SMART; SM00401; IGCli 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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GC3M_MOUSE
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SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                      CF7F264B50A41B95 CRC64;
                                                                                                                                                                      (POTENTIAL).
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POTENTIAL.
CYTOPLASMIC (POTENTIA E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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64.7%; Pred. No. 4e-71;
tive 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Iggamma-2A chain C region, A allele.
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                      Alternative splicing
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es 213; Conserv
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                 Transmembrane; PNON_TER 1 DOMAIN 1 DOMAIN 98 DOMAIN 114 DOMAIN 224
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P01863;
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Best Local S:
Matches 213,
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CONFLICT
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SEQUENCE
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EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
MEDLINE-81223894; PubMed-6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                                                                                                              Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.9%; Score 1129; DB 1; Length 330; 63.9%; Pred. No. 1.5e-70; ive 43; Mismatches 73; Indels
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                                                               Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Immunoglobulin C region.
                                                                                      MYELOMA PROTEIN MOPC 173.
MEDLINE-74175517; Pubmed-4831970;
                                                                                                                                                                                                      MEDLINE=73056887; PubMed=4565406;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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82
107
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                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=88166903; PubMed=3127222;
MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Calfre P., Waldmann H., Calabi F.;
Sequence a rat immunoglobulin gamma 2c heavy chain constant region cDNN: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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      Immunoglobulin domain;
      Immunoglobulin C region.

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Pred. No. 1.9e-70;
1; Mismatches 66
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
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                              299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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62.8%; Pred
tive 51;
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HSSP; PD1857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity
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15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                437
                                      ||:|:||:||||||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
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LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
IS-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotyplc forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                  378 REEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLIVDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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PIR; A02153; G2MSAB.
HSSP; P01857; 1FC1.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAB_MOUSE
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GCAB_MOUSE
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Score 1126.5; DB 1; Length 335; Pred. No. 2.3e-70;

44.8%; 61.6%;

Query Match Best Local Similarity

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141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                    315 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
Gaps
                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK-----SCDKTHTCPPCPA
                                                                                                                                                                                 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                 375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
7;
Indels
70;
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                                                                                                                                                                                                                                                                                                                                                                                                       435 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Mismatches
52;
Conservative
Matches 207;
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Search completed: August 14, 2002, 15:23:14 Job time: 687 sec

us-09-499-662-143.rsp

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August 14, 2002, 15:22:15; Search time 187.61 Seconds (without alignments) 433.386 Million cell updates/sec
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2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                         BLOSUM62DX
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_bacteriap:*
sp_archeap:* 99: 100: 112: 114: 116: 116:

sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*

sp_fungi:*
sp_human:*
sp_invertebrate:*

SPTREMBL_19:* 1: sp_archea:* 2: sp_bacteria:*

Database :

sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*

	Description	Q9d814 mus musculu		Q99125 mus musculu	mus	Q9r1a4 mus musculu	Q91z05 mus musculu	Q95m34 equus cabal	Q96pq8 homo sapien	0921k1 mus musculu	Q96qa6 homo sapien	O91wt3 mus musculu	Q9brv0 homo sapien	Q91wt1 mus musculu	-		уошоч
SUMMARIES	QI	Q9D8L4	Q99LC4	Q99L25	Q99L31	Q9R1A4	091205	Q95M34	096PQ8	Q921K1	Q96GA6	Q91WT3	Q9BRV0	Q91WT1	Q91WR1	Q96BB9	096DK0
	Query Match Length DB	73 11	63 11	73 11	68 11	37 11	473 11	37 6	01 4	78 11	14 4	81 11	00 4	81 11	88 11	97 4	96 4
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dф	Query	65.1	64.7	63.1	62.1	57.(	56.4	50.	49.6	39.5	36.8	35.4	34.1	33.7	32.6	32.3	31.9
	Score	1639.5	1628.5	1588.5	1562	1433.5	1420.5	1263.5	1257	986	927.5	890.5	859	836.5	820	812.5	804
	Result No.	1	7	m	4	5	9	7	80	6	10	11	12	13	14	15	16

homo homo homo homo		096kx8 homo sapien 09dcd9 mus musculu 09pp6 homo sapien 091v67 mus musculu 092499 momo sapien 099298 homo sapien	092473 mus musculu 095978 homo sapien 092495 mus musculu 092478 mus musculu 092495 mus musculu 092497 mus musculu 092497 mus musculu 092497 mus musculu 092496 mus musculu
4 Q9BU10 4 Q9BQB8 11 Q99LA6 4 Q96AA6 4 Q96AA6	4 Q96EY0 11 Q99KA4 11 Q91WP5 11 Q91Z07 11 Q91XE1 11 Q99K22	4 Q96KX8 11 Q9DCD9 11 Q9NPP6 11 Q91V67 11 Q924P9 4 Q9Y298 11 Q924Q2	11 092483 11 092483 11 092405 11 092488 11 0924P5 11 0924P6 11 092407 11 092400
597 484 618 494	613 4487 486 488 479	496 426 1149 1150 1423	1443 1445 1443 1443
30.1 30.1 29.1 29.2	29.1 28.8 27.8 27.8 26.1	25.5 24.0 21.6 20.9 20.9	2002 2001 2002 2009 2009 2009 2009 2009
762.5 758.5 758.5 752.5	732 724.5 718.5 700 689.5 656	641 605 580.5 542.5 530.5 525 517	513.5 498.5 496.5 496.5 495.5 491.5 489.5
17 18 19 20 21	222 222 232 232 232 232 232 232 232 232	29 33 33 34 35 35 35 35 35 35 35 35 35 35 35 35 35	00000000000000000000000000000000000000

## ALIGNMENTS

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InterPro; IPR003006; Ig_MHC
                                                                                                                                          Best Local Similarity 63.8%
Matches 301; Conservative
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SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                                                                                                         61 GOGLEWMGEIDPSDSYTNYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                         181 WNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                      241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
                                                                                                                                                                                                                                                                                                                                                                                                                           297
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                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  38 RVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.1%; Score 1639.5; DB 11; Length 473; 63.9%; Pred. No. 8.2e-129; 1ve 69; Mismatches 94; Indels 9;
## MGD; MGI:96443; Igh-1.
## InterPro; IPR003599; Ig.
## InterPro; IPR003509; Ig_like.
## InterPro; IPR003600; Ig_like.
## InterPro; IPR003606; Ig_MHC.
## InterPro; IPR003596; Ig_W.
## Pfam; PF00047; Ig, 4.
## SMART; SM00409; IG, 2.
## SMART; SM00409; IG_Like; 1.
## SMART; SM00410; IG_Like; 1.
## SMART; SM00410; IG_Like; 1.
## PROSITE; PS00290; IG_MHC; UNKNOWN_1.
## PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                Matches 304; Conservative
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Best Local Similarity
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61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSYD-LFAYWGOGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP 238
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                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        64.7%; Score 1628.5; DB 11; Length 463; 63.8%; Pred. No. 6.6e-128; ive 71; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC003888 AAH03888.1;
HSPP: P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00290; IG_l1ke; 1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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96352328B3332ADB CRC64;

51661 MW;

AA;

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NON_TER
SEQUENCE
    SECUENCE
                                Query Match
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Q9R1A4;
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                                                                                                                                                                                                                                TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                       238 VEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                              VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
                                                                                                                                                                                                                                                                                                                                                     EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
                                                                                          Gaps
                                                                                                                                                   GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                        1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                        ERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYK
                                                                                                                                                                                                                                                                                                                                                                                           63.1%; Score 1588.5; DB 11; Length 473; 63.6%; Pred. No. 1.5e-124; ive 60; Mismatches 106; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.,

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

Bubli BC003878; AAH03878.1; -

R HSSP: P01842; 7FAB.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003500; Ig_like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003306; Ig_WHC.

InterPro; IPR003306; Ig_V.

R InterPro; IPR003596; Ig_V.

R FABRT; SM00407; IGc.1; 3.

SMART; SM00410; IGc.1; 3.

SMART; SM00410; IG_like; 1.

SMART; SM00410; IG_like; 1.
SMART; SMO0407; IGC1; 3.
SMART; SMO0406; IGV; 1.
SMART; SMO0410; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 473 AA; 52449 MW; BE9889BT986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09121;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                         Conservative
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                                                                               Similarity
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                                                                               Best Local Sim
Matches 302;
                                                                      Query Match
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SEQUENCE FROM N.A.

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal antibody (Amb 7, its 11ght and heavy chains) and construction of a single chain antibody (ScFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF153372; AAD40443.1;

InterPro: IPR003606; Ig_like.

InterPro: IPR003606; Ig_MHC.
                                                                                                                                                                                               358
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                                                                                                                                                                          GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYCARNRD 120
                                           Gaps
                                                                                    9
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                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                               WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                        YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Sciurognathi; Muridae; Murinae; Mus
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9
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  468;
  Length
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
MUS musculus (Mouse).
; Score 1562; DB 11;
; Pred. No. 2.5e-122;
61; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
62.1%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; 19; 4. SMART; SM00406; IGv; 1. SMART; SM00410; IG_like; 2.
                      Best_Local Similarity 62.9
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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437 AA;
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185
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                       7;
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2
                                                                                                  228 --SSVFIFPPREMEMDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 285
                                                                                                                                                                                                                                                                               81 QKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVSS 140
                                                                                                                                 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                              201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 MGEIDPSDSYTNYNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 -- FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 184
                                                       Gaps
                                            21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNYN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEW 66
                                                                                                                                                                                         Mus musculus (Mouse).
Wataryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                              379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                       17;
 DB 11; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.4%; Score 1420.5; DB 11; Length 56.9%; Pred. No. 1.7e-110; ive 75; Mismatches 114; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327, AAH10327.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51946 WW, CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 091205 PRELIMINARY; PRT; 473 AA. 091205; 1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 51.9 KDA PROTEIN.
                       96;
           Pred. No. 1.3e-111;
57.0%; Score 1433.5;
59.1%; Pred. No. 1.3e
                    72; Mismatches
                                                                                                                                                                                                                                                                                                                                                         439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                     267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 56.9
269; Conservative
           Similarity
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 Query Match
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wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
Corporalization of the equine immunoglobulin heavy chain constant region
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
NON_TER 1 1
SEQUENCE 337 AA; 37438 MW; A6OBF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                          254
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                                                                                                                               ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD
                             141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTIAPKVFALAPGCGTISDSTVALGCLVSGYFPEPVKVSWNSGSLISGVHTFPSVLQSS
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                                                                                                                                                                                                           FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metażoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                   418 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                              421 APVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.2%; Score 1263.5; DB 6; Best Local Similarity 68.9%; Pred. No. 1.4e-97; Matches 233; Conservative 44; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-98383416; PubMed-9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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01-DEC-2001
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Indels Length

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YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDWTWRILFLYAAAATDAYSQMQLYQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAP 60
                                                                                          GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                            181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TKVDKRVEPKS------CDKTHTCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.8%; Score 927.5; DB 4;
36.6%; Pred. No. 4.3e-69;
tive 85; Mismatches 166;
   Score 986; DB 11;
Pred. No. 1.8e-74;
; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JNKNOWN (PROTEIN FOR MGC:15420).
                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
   39.2%;
67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PCPAPELLGGPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.8'
Best Local Similarity 36.6'
Matches 211; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                      187;
   Query Match
Best Local 8
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Targeting tissue factor on tumor vascular endothelial cells ar cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL: AF272774; AAKS66661; -. SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHFALHNHYTQKSLSLSPGK 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 701;
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelé
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                               096P08;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.9%; Score 1257; DB 4;
99.1%; Pred. No. 1.4e-96;
tive 2; Mismatches 0;
                                                                                          LIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21477448; PubMed=11593034;
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Matches 230; Conservative
                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Z., Garen A.;
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Euteleostomi;

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Gaps

Indels 115; Length 614;

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Q921K1;

**0921K1** 

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RESULT Q921K1

us-09-499-662-143.rspt

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PROSITE; PS00290; IG_ike; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 500 AA.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R InterPro; IPR003597; Ig_c1.
R InterPro; IPR003060; Ig_like.
R InterPro; IPR003065; Ig_MHC.
R InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00406; IGv; 1.
PROGRAMMED:
R SMART; SM00410; IG_like: 1.
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Best Local Similarity 41.15
Matches 206; Conservative
                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                             (Human)
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                                                                                                                                         475
                   -----VELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                 PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
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                                                                                                                                                                                                       SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 IEKTISKAKGOPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-COLON;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOLON;
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     v1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
HYPOTHETICAL 52.0 KDA PROTEIN.
BINE MUSCULUS (Mouse)
                                                                                                                                                                                                                                                                                     431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207; Conservative
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Matches 20
                                                                                                                                                                                                                                                                                                                                                             RESULT 11
Q91WT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HINDER STREET HINDER STREET HINDER STREET HINDER STREET HINDER STREET 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK--------DTLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-PROSTATE;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.1%; Score 859; DB 4;
41.1%; Pred. No. 1.7e-63;
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               PRELIMINARY;
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 LSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || |
IDRLSGK 470
                                                                                                                                                                           TISSUE=KIDNEY;
Strausberg R.;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 192;
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               091WR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    091WT1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 NCPGICSPPTTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                   33.2%; Score 836.5; DB 11; Length 40.5%; Pred. No. 1.3e-61; Live 72; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
Hypothetical protein.
SEOUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                                                               481
                                                                                                                                                 PRT;
                                                                  | ||||| :||:: ||
462 VGHEALPLAFTQETIDRLAGK 482
                                                   450 VMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.2%
Best Local Similarity 40.5%
Matches 195; Conservative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 GK 470
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395
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121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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O. DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 53.0 KDA PROTEIN.
MAIN musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musines; Muslanteleostomi; MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 QELNVNCPGICSPPITPPPPSCO----PSLSLQRPALED-LLLGSDASITCTLNGL--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013539; AAH13539.1; -. Hypothetical protein. S2964 MW; F12068460B400B9D CRC64; SEQUENCE 488 AA; S2964 MW; F12068460B400B9D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 820; DB 11; 11 39.4%; Pred. No. 3.1e-60; Conservative 84; Mismatches 177;
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18;
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                                                                                                                                                                                                                                                                                                                                                               176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                 120 DYSNNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSCIILFIVATATGVHSOVOLVQSGAEVKRPGASVKVSCKASGYTFTSYMMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 N-----TKVDKRVEPKS------CDKTHTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSOSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF
                                                                                                                                                                          Query Match 32.3%; Score 812.5; DB 4; Length 597;
Best Local Similarity 32.5%; Pred. No. 1.7e-59;
Matches 189; Conservative 95; Mismatches 179; Indels 119;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                             SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strauaberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Search completed: August 14, 2002, 15:22:16 Job time: 684 sec

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(without alignments)
226.770 Million cell updates/sec
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                                                                                                      August 14, 2002, 15:15:37; Search time 230.21 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		% Ouerv				
No.	Score	Match	Match Length DB	BB	ID	Description
-	2517	100.0		21	AAW90934	Humanised anti-F
7	2515	6.66		21	AAW90933	Humanised anti-F
3	2512	93.8	470	19	AAW83037	Anti-Fas humanis
4	2512	93.8		21	AAB14779	Humanised anti-F
ß	2512	8.66		23	AAW90929	Humanised HFE7A
9	2512	8.66		21	AAW90935	Humanised anti-F
7	2499	99.3		19	AAW83036	Anti-Fas humanis
80	2499	99.3		21	AAB14776	Humanised anti-F
6	2499	99.3		21	AAW90926	Humanised HFE7A
10	2497	99.5		21	AAW90936	Humanised HFE7A
11	2348.5	93.3		22	AAM52156	Humanised HMFG-1

(SANY ) SANKYO CO LTD.

Humanised HMFG-1 h	HMFG-	HMFG-	HMFG-		in of		Humanised 323/A3 (		Chimeric 2403 IgG	Monoclonal antibod	Sequence of antibo	Human reshaped F19	Antibody D heavy c	Ganglioside GM2 an	Completely humanis	Amino acid sequenc	Human immune syste	nti	Humanised anti-IL-	Humanised anti-IL-	Chimeric mouse/hum	Amino acid sequenc	Anti-IL-8 humanise	nove c	Anti-5T4 single ch	Human type antihum	Human type antihum		type	O)	MoTAbII fusion pro	Human type antihum	Reshaped CAMPATH-1
AAM52159	AAM52158	AAM52161	AAM52157	AAM52160	AAW48650	AAB72228	AAB72232	AAB08026	AAE03755	AAW88464	AAR24442	AAY50166	AAR31023	AAB83156	AAR43339	AAW49816	AAB36210	AAY 29458	AAB30322	AAY77766	AAY50157	AAB83838	AAW69316	AAU14177	8	47	AAG64471	AAG63640	AAG64469	AAW85689	9	^	AAR22757
22	22	22	22	22	19	22	22	21	22	20	13	20	14	22	14	19	22	20	21	21	20	22	19	22	20	22	22	22	22	20	20	22	13
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthatic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthiitis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed heavy chain Heu 2 protein. AAW90934 standard; Protein; 470 AA 98JP-0276881. 98JP-0276882. 99EP-0307711 08-AUG-2000 (first entry) 39-SEP-1999; 30-SEP-1998; 30-SEP-1998; 05-APR-2000. EP990663-A2 Synthetic. AAW90934; AAW90934 

Takahashi T; Tamaki I, Nakahara K, Ή, Haruyama Serizawa N,

WPI; 2000-258930/23. N-PSDB; AAA11645 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

263pp; English. Claim 2 ; Page 174-176;

Interior describes a nover numerized anti-ras antibody like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas indead system, by bindibiting binding between fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive (inhibition of ligand binding. (I) are used to treat and/or prevent clubes exphematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autohimune hemolytic anemia, sterility, mysathenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fase, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic murine disease models. (I) act on the active site of Fas, i.e. they minic murine disease models. (I) act on the active site of Fas, i.e. they minic murine a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention. This invention describes a novel humanized anti-Fas antibody-like 

470 AA; Sequence

ö 100.0%; Score 2517; DB 21; Length 470; llarity 100.0%; Pred. No. 4.4e-143; Conservative 0; Mismatches 0; Indels 0; Similarity Best_Local Sim Matches 470; Query Match

9 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP

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GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 61 δ

YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 g δ

WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240 181 181 õ g

g

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 δ g

301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360 301 gg ç

KAKGOPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420 361

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. 361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420 Humanised anti-Fas designed heavy chain Heu 1 protein. Æ. AAW90933 standard; Protein; 470 98JP-0276881. 98JP-0276882. 99EP-0307711. 08-AUG-2000 (first entry) 29-SEP-1999; 30-SEP-1998; 05-APR-2000. EP990663-A2 Synthetic. AAW90933; AAW90933 RESULT g ŏ 셤 A STATE OF COLORO COLOR

30-SEP-1998;

(SANY ) SANKYO CO LID.

Takahashi T; Nakahara K, Tamaki I, Serizawa N, Haruyama H,

WPI; 2000-258930/23. N-PSDB; AAA11644.

treating or preventing e.g. apoptosis selectively in New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents oppotosis in cells with a normal system, by inhibiting batween Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-anemic, anti-allergic, anti-arthiritic, antivaral, anti-arthiritic, antivaral, cartiarthritic, antivaral, anti-arthiritic, antivaral, cartiarthritic, cardiant and hepatropic activity. (1) induce antiarterisoclerotic, cardiant and hepatropic activity. (1) induce antiarterisoclerotic, cardiant and hepatropic activity. (1) induce antiarterisoclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, soleroderma, Goodpature syndrome, Crohn's anemia, Addison's disease, scleroderma, Goodpature syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B. C or D) or alcoholic), and transplant rejection. (I) selectively

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inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                       361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombopenia purpura; insulin-dependent diabetes; allergy; actopy; atterlosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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Pred. No. 5.8e-143;
1; Mismatches 0;
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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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Tohru
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                       20..470
/label- Mat_protein
20..140
/label- Variable
Location/Qualifiers
                'label Sig_peptide
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S, Shin Y,
                                                         141..464
/label- Constant
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/label= CDR_H2
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25-JUN-1997;
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DB 19; Length 470;

Score 2512; DB 19; Pred. No. 8.8e-143;

99.88;

Best Local Similarity

Query Match

Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the diseases caused by an abnormality autoimmune diseases, contains
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                                               GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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Indels
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Mismatches
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5:
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Conservative
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- Homo sapiens.
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468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
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The invention relates to compositions for the prevention or treatment containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-artictic; antiviral; immunodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antirheumatic; anti-Fas; nephrotropic; antilnfertility; neuroprotective; antiarteriosclerotic; nephrotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2512; DB 21;
Pred. No. 8.8e-143;
2; Mismatches 0;
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Best Local Similarity 99.6%;
Matches 468; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 AA;
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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
capptosis in cells with a normal system, by inhibiting binding between
capptosis in cells with a normal system, by inhibiting binding between
capptosis in cells with a normal system, by inhibiting binding between
canti-indiamatory, darmatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
cantiartisoclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
colls surfaces associated with the Fas/Fas ligand system, especially systemic
cutions of ligand binding in syndrome, permicious or hypoplastic
canemia, Addison's disease, scleroderma, sterility, myasthenia gravis,
calisase, autoimmune hemolytic anemia, sterility, myasthenia gravis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
cells. They bind to both human and murine Fas, so can be evaluated in
centis the apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
centis the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
ca humanised anti-marine antibody response. This sequence represents
can humanised anti-marine disease, antibody HEFAA designed heavy chain which is used in
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Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenta purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example reference 22; Page 150-152; 263pp; English.
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2; Mismatches
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ilarity 99.6%;
Conservative 2
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Matches 468; Conser
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                                                                                                                                                                                                   Synthetic
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anti-allergic; anti-arthritic, antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
                                                                                                              241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv
                                                                                                                                                                              YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                               KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                               WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi T;
                                                                                                                                                                                                                                                                                                                             LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas designed heavy chain Heu 3 protein.
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98JP-0276882.
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N-PSDB; AAA11646.
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30-SEP-1998;
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continuous in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apportosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding (I) are used to treat and/or prevent classase associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernoious or hypoplastic versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cardiomyopathy, glomerulonephritis, hepatis (fulminant, chonic, viral cardiomyopathy, glomerulonephritis, hepatis (fulminant, cardiomyopathy, glomerulonephritis, hepatis (fulminant, cells), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in mormal endisease models. (I) act on the active site of Fas, i.e. they minic murine disease models. (I) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
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470 AA; Sequence

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                                                                                                                  61 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrsedtavyycarnrd 120
                                                                                                                                                                                                                                    241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                       Gaps
                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                   121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                      181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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Length 470;
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Score 2512; DB 21;
Pred. No. 8.8e-143;
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                       2; Mismatches
99.8%;
99.6%;
                      Matches 468; Conservative
           Local Similarity
Query Match
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Anti-Fas humanised antibody HFE7A heavy chain.

HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.

Homo sapiens. Synthetic.

20.470 /label= Mat_protein /label= Sig_peptide Location/Qualifiers 20..140 /label- Variable 141..464 /label= Constant "claim 9" "claim 9" 50..54 /label= CDR_H1 /label= CDR_H2 CDR_H3 118..129 /label= Cl /note= /note= Peptide Protein Region Region Region Region Region

/note= "claim 9"

AU9859701-A 08-OCT-1998 98AU-0059701 30-MAR-1998;

97JP-0276064. 97JP-0082953. 97JP-0169088. 08-OCT-1997; 25-JUN-1997; 01-APR-1997; 

(SANY ) SANKYO CO LTD.

Jun O, Kimihisa I; , Tohru T; Hiroko Y, Ju S, Shin Y, Nobufusa Hidevuki H. Masahiko O, Akio S.

WPI; 1998-543440/47. N-PSDB; AAV70079

used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, New antibodies and proteins bind conserved epitope of Fas antigen myocarditis, hepatitis and AIDS

Claim 22; Page 212-213; 292pp; English.

This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. coll pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human IgG1 constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also

AAW83036 standard; Protein; 470 AA.

AAW83036

RESULT

(first entry)

15-MAR-1999

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AAW83036;

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30-SEP-1999;
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                                                                                                                                                                                                                                                          GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                            121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia. Addison's disease, scleroderma, Goodpasture syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin'dependent diabetes), allerqise, atopy, arteriosclerosis, anyocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                     KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
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                                                                                                                                                    99.3%; Score 2499; DB 19; 99.1%; Pred. No. 5.3e-142; ive 2; Mismatches 2;
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                                                                                                                                                                            Conservative
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Chimeric - Homo sapiens.
                                                                                                                                                                Similarity
                                                                                                                     470 AA;
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Matches 466;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                                                                                                                Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
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                                                         98JP-0276883
99JP-0278301
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Matches 466; Conservative
                                                                                                                  (SANY ) SANKYO CO LTD
                                                                                                                                                                              WPI; 2000-485645/43.
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                                                                                                                                                                                                                                                                                                                                   anti-Fas antibody
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5.3e-142;

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Conservative

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Similarity

181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60  361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv

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AAW90936 standard; Protein; 470 AA.

RESULT 10

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AAW90936

(first entry)

08-AUG-2000

AAW90936;

421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

361 KAKGOPREPQVYILPPSREEMTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPV 

YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS

301

Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allargic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepartotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; systemic lupus erythematosus; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Tamaki I, Takahashi T; Humanised HFE7A designed heavy chain protein. cells with abnormal Fas-Fas ligand systems Nakahara K, AAW90926 standard; Protein; 470 AA. 99EP-0307711. 98JP-0276881. 98JP-0276882. (first entry) Serizawa N, Haruyama H, (SANY ) SANKYO CO LID. WPI; 2000-258930/23. N-PSDB; AAA11597 08-AUG-2000 39-SEP-1999; 30-SEP-1998; 30-SEP-1998; 05-APR-2000 EP990663-A2 Synthetic. AAW90926;

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in

Example reference 15; Page 134-136; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between the apoptosis in antidiabetic, anti-allergic, anti-arthritic, antiviral, continuatic, antidiabetic, antiminentality, neuroprotective, antinineuratic, nephrotropic, antiminertility, neuroprotective, antinineuratic, nephrotropic, antiminertility, neuroprotective, antiminertility immunosuppressive, thyromimetic, antimineuratic cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capptosis by binding to cell surface Fas or inhibit it by competitive inhibits apoptosis by binding to cell surface system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, cleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, antiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in cardine disease models. (I) act on the active site of Fas, i.e. they minic inducing a human anti-murine antibody HESPA designed heavy chain which is used in the method described in the invention.

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470

Sequence

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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclarotic; anti-Fas; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                          antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                        Humanised HFE7A designed heavy chain HHH type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-0276881.
98JP-0276882.
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-damentoly anti-arthritic, anti-inflammatory, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit to prompetitive inhibition of ligand binding. (I) are used to treat and/or prevent cinhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent anamia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's corrus host disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, mysthania gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arterlosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the nutive ligand, do not induce liver disease, and have reduced risk by human anti-murine antibody response. This sequence represents which is adearnibed in the antivordice in the active site of Fas, i.e. they mimic which is a dearnibed.
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                    Takahashi T;
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                    Tamaki I,
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Pred. No. 7e-142;
; Mismatches 2
                                                                                                                                                                    cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                  Claim 2; Page 188-189; 263pp; English.
                    Nakahara
                                                                                                                           New humanized anti-Fas antibody,
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                    Нагиуата Н,
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                    Serizawa N,
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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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26-MAR-2001; 2001WO-GB01324.
                          03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
                                                                       LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                       (ANTI-) ANTISOMA RES
                                                                                                                                 WPI; 2001-662969/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          731 AA;
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Matches 437;
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181 181 241 301 301 361

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytocoxic portion having endonucleolytic activity, exemplified by AAM52154.368 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic epithelial mucin; PEM1;
I; human; cytostatic; cancer; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity follymorphic epithelial mucin, and cytotoxic portion having endouncleolytic activity
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                                                           Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
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93.0%; Pred. No. 8.8e-133;
iive 20; Mismatches 10;
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cytotoxic; endonuclease; DNase
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apoptosis.
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301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                    KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                            Humanised monoclonal antibody; polymorphic epithelial mucin; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer;
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                                                                                                                                                                               LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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02-OCT-2000; 2000US-237159P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endonucleolytic activity
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Synthetic.
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DB 22; Length 741;

93.3%; Score 2348.5; DB 2: 93.0%; Pred. No. 8.9e-133; ive 20; Mismatches 10;

Conservative

Similarity

Local Simi hes 437;

Best Loca Matches

Query Match

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Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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02-OCT-2000; 2000US-237159P.
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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
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I; human; cytostatic; cancer; apoptosis.
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                                                                              Length 729
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                                                                               DB 22;
                                                                              93.1%; Score 2343.5; DB 2 93.0%; Pred. No. 1.7e-132;
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2000US-237159P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymorphic epithelial mucin; PEM1;
I; human; cytostatic; cancer; apoptosis.
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                    comprising humanised monoclonal antibody having specific popolymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                            Score 2343.5; DB 2. Pred. No. 1.8e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                     Claim 20; Figure 12; 176pp; English.
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cytotoxic; endonuclease; DNase
                                                                                                                                                                                                                                                                                                                                                                                            93.1%;
93.0%;
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2001-662969/76
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                                                                                                                                                                                                                                                                                                                                      739 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
                                                                                                                                                                                                                           Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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                                                                                                                                                                                                                                                                                           Claim 20; Figure 8; 176pp; English.
                                                                                                      2000GB-0008049.
2000US-237159P.
                                                                             26-MAR-2001; 2001WO-GB01324
                                                                                                                                               (ANTI-) ANTISOMA RES
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Matches 435; Conser
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                         WO200174905-A1
                                                                                                      03-APR-2000;
02-OCT-2000;
                                                    11-OCT-2001
 Synthetic.
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Search completed: August 14, 2002, 15:15:38 Job time: 836 sec

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Sequence 9, 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARET APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.7%; Score 2232; DB 2;
Best Local Similarity 88.7%; Pred. No. 5.2e-159;
Matches 422; Conservative 20; Mismatches 28;
US-09-679-397-2
PCT-US93-07832-23
US-08-437-642B-23
US-08-127-101A-7
US-08-127-101A-7
US-08-127-101A-7
US-08-049-672A-4
US-08-397-411-7
US-08-487-550-4
US-08-461-550-4
US-08-461-968A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEX: (202) 783-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ROTHWELL, FIGG, ERNST 6
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/FB_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/FCTUS_COMB.pep:*
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Compugen Ltd
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US-09-049-672A-8

US-09-048-71

US-09-485-737B-67

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US-09-485-737B-67

US-08-437-642B-22

US-08-437-642B-22

US-08-437-642B-22

US-08-437-642B-22

US-08-45-8

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US-09-296-005-14

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US-08-466-163B-8
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Title: Perfect score:

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                                                                                 120 ----DYSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 174
                                                                                                                                          EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 234
                                                                                                                                                                                                 DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
                                                                                                                                                                                                                                                          EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
1 MDWTWRFLFVVAAATGVQSQMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVRQAP
                          61 GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNR-
                                                                                                                                                                                                                                                                                                                                355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/458,516 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 449 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
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linear
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STRANDEDNESS:
TOPOLOGY: line
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119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
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                                                    Gaps
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                                                                                                    20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY
                                                                                                                                                                                                                                                                                                             140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
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APPLICANT: Tang, Y. Tom
APPLICANT: Tue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
     Length 449;
                                                  Indels
Query Match 88.6%; Score 2230; DB 1; Best Local Similarity 92.9%; Pred. No. 6.8e-159; Matches 419; Conservative 15; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 2.0
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STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TOPOLOGY: Linear
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US-09-026-985-71
                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                   127 FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
                                                                                                                                                                                                                                                                                                                                                                 7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEW 66
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 713 / Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Genzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESSED ADDRESS:
ADDRESSEE: Generitech, Inc.
STREET: 1 DNA WAY
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                                                                                                                                                                                                                                                                                                 Length 467;
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                                    NAME: CETTONE, MICHAEL C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-865-0555
TELEFAX: 650-845-4166
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                             INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                              Query Match 87.4
Best Local Similarity 89.0
Matches 413; Conservative
                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                         ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
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US-09-027-449-71
                                                                                                                     TELEX:
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NOKFKGRETLSRDNSKNTAYLOMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.3%; Score 2198.5; DB 3
89.8%; Pred. No. 1.5e-156;
live 28; Mismatches 17;
                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                               PRIOR ADPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-3an-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9891
INFORMATION FOR SEQ ID NO: 71:
SEQUETERING
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 452 amino acids
Amino Acid
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APPLICANT: BUYSE, MATIE-Ange.
APPLICANT: SABLON, ETWIN
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US 409485,737B
CURRENT PILING DATE: 1998-06-14
PRIOR PILING DATE: 1998-06-14
PRIOR FILING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 104
SSO ID NO 67
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.5%; Score 2177; DB 4;
88.2%; Pred. No. 6.5e-155;
live 20; Mismatches 31;
     Sequence 67, Application US/09485737B
Patent No. 6350860
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.5% Best Local Similarity 88.2% Matches 410; Conservative
                                                                                                                                                GENERAL INFORMATION:
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US-09-485-737B-90
                                                                                       US-09-485-737B-67
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                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 452;
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89.8%; Pred. No. 1.5e-156;
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disconnettible
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION:
TELEPHONE: 650/225-5530
Sequence 71, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
                                                                                                                                       NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 452 amino acids
Amino Acid
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US-09-026-985-71
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                                                                                                                                                                                                                CITY: S
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQ 362
                                             Gaps
                                                                                      6 IILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLE 65
                                                                                                            126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
                                                                                                                                                                                                                                                                                                                                                                                             246 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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                                           4;
Length 468
                                           Indels
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E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               CURRENT APPLICATION DAMA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION NUMBER: US/07/934,373C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
Genentech, Inc.
               South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 85.8%; Local Similarity 89.2%;
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                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                        OPERATING SYSTEM
  ADDRESSEE:
                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                COUNTRY:
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                                 APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT APPLICATION NUMBER: POT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
SEQ ID NO 90
LENGTH: 71

**LENGTH: 71
**CHARTH: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 WMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.5%; Score 2177; DB 4; Length 711; 88.2%; Pred. No. 1.1e-154; 1ve 20; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
WIMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/07934373C Patent No. 5821337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: SYNTHETIC US-09-485-7378-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.2
Matches 410; Conservative
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137 TVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436 80 NQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136 Gaps 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79 3, Indels ; Score 2159.5; DB 2; ; Pred. No. 1.3e-153; 18; Mismatches 28; KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470 

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241 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
                                                                                                                                                                       301 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 NQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                   SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                  EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-r--
CIPDOT SYSTEM: PC-DOS/Ms-r--
CIPDOT DA++-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.8%; Score 2159.5; DB 98st Local Similarity 89.2%; Pred. No. 1.3e-153.
Matches 405; Conservative 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
OCRRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                     437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                           421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
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APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMBER: 07/934373
21-AUG-1992
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 454 amino acids
amino acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                        RESULT 10
PCT-US93-07832-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 NOKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
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ZIP: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINDEATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
: ...TUTG DATE: 09-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2159.5; DB 3 Pred. No. 1.3e-153;
                                     Sequence 22, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US92/05126
APPLICATION NUMBER: DCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTURNET, DEAD, WENDER:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P070;
TELECHMUNICATION INFORMATION:
TELEPAX: 650/255-1994
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TTPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/934373
FILING DATE: 21.AUG-1992
PRIOR APPLICATION DATA:
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FILING DATE: 17-NOV-1993
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89.2%;
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STATE: California
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Best Local Similarity 89.2<sup>3</sup>
Matches 405; Conservative
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US-08-437-642B-22
                      US-08-437-642B-22
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                                                                                                            LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                             EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
                                                                                                                                                                                                                                                                                                          377 SREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLTVD 436
                                                 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BELMAN, LENA
APPLICANT: RACZOREK, MICHEL
APPLICANT: RACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
ITILE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: 25
CORRESPONDENCES: 25
CORRESPONDENCES: 25
ADDRESSEE: D.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450

FILING DATE: US/08/793,450

CLASSIFICATION: 536

PRIOR APPLICATION TS
APPLICATION NUMBER: FF 94/10566

FILING DATE: US-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08793450 Patent No. 6312690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Sequence 14, Application US/08887352B

Sequence 14, Application US/08887352B

Patent No. 5994511

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
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                                                                                                                                                                                                                                                                 1 MGWSCIILFLVATATGVHSQVQLEQWGAGLIKPSETLSLTCTYYGGSFSGYYWSWIRQPP 60
                                                                                                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
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     Length 472;
                                                                                                      Indels
85.3%; Score 2146; DB 4;
85.1%; Pred. No. 1.4e-152;
iive 26; Mismatches 37;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: HOP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELEPHONE: 650/255-1489
TELEPHONE: 650/255-1489
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CITY: South San Francisco
STATE: California
COUNTRY: USA
     Query Match 85.39
Best Local Similarity 85.19
Matches 404; Conservative
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: 650/225-1489 650/952-9881

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TELECOMMUNICATION INFORMATION:
                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                               139
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                 60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119
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                                                                                                                          84.5%; Score 2126; DB 2; Length 451; 87.8%; Pred. No. 4e-151; Live 23; Mismatches 30; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfratin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
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FILLME DATE: 03-01-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODOda, Craig 6.
RECISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
                 LENGIH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                             Best_Local Similarity 87.8
Matches 397; Conservative
SEQUENCE CHARACTERISTICS
                                                ; TOPOLOGY: Linear
US-08-887-3528-14
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                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
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                                                                         Length 451;
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                                                                       84.5%; Score 2126; DB 2;
87.8%; Pred. No. 4e-151;
iive 23; Mismatches 30;
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin //_____
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STATE: Californ's
                                                                     Query Match
Best Local Similarity 87.8
Matches 397; Conservative
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APPLICATION NUMBER:
FILING DATE:
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; TOPOLOGY: Linear
US-08-887-352B-16
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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQGLEWMGEIDPSDSYTN 78
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                            CURRENT APPLICATION NUMBER: US/09/109,207
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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     P1123R1
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LENGTH: 451
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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87.8%; Pred. No. 4e-151;
ive 23; Mismatches 3
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                                                                                                PILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/879495
FILING DATE: 0/-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 0/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
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US-09-109-207C-14
Sequence 14, Application US/09109207C
Patent No. 617213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
TITLE OF INVENTION: Improved Anti-ig
                                                   FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P07
TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-1489
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Amino Acid
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Best Local Similarity 87.85
Matches 397; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                 OM protein - protein search, using sw model
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August 14, 2002, 15:19:00; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec Run on:

US-09-499-662-145 2517 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Perfect score: Sequence: Scoring table:

283138 seqs, 96089334 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	In gamma-1-chain	gamma - 3	qamma-3	q qamma-2a chain	gamma-2 c		Ig gamma-2b chain				qamma -		G	Ig gamma 2a chain	ь	ф		gamma	Ig gamma chain C r		Ig gamma-2 chain C	Ig heavy chain C r	gamma-	qamma-1	gamma-3		gamma-2b	gamma-1 c	
SUMMARIES	QI	Сини	A23511	A60764	537483	G2HU	G4HU	G2MS11	S40295	S01321	S22080	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	G1MS	PS0018	G1MSM	G3MSM
	DB	7	7	7	7	7	-	-	N	~	~	7	~	7	~	7	4	~	7	Н	~	-	7	П	~	7	-	7	_	П
	Length	330	377	377	469	326	327	474	446	475	470	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
dР	Query	69.8	65.1	65.1	64.0			61,5	61.4	59.7	58.6	58.4						49.5		•	48.9		46.3		45.9	45.7	45.5	45.5	45.3	45.3
	Score	1758	1639.5	1637.5	1611.5	1610	1599.5	1547	1545	1502.5	1476	1469	1434	1428.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
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Iq qamma-2a chain		Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c		Ig Y heavy chain (
G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	G2MSBM	147162	S38864	S14683	S04845	S69131	<b>S</b> 38950	A49444	S69340	B46529
Н	7	П	Н	7	~	Н	7	7	7	7	7	7	7	7	7
330	329	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.7	37.5	36.8	34.4	33.8	31.7	30.4	30.3
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	866	945	927.5	866.5	852	797	764.5	761.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1 GHHU
Ig gamma-1 chain C region - human
 C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Kes. 10, 40/1-40/9, 1982 A:Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A, Rererence number: A93433; MULD:822/4238 A, Accession: A93433
A;Molecule type: DNA A;Residues: 1-330 <ell></ell>
A;Cross-references: EMBL:Z17370 A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
•
submitted to the EMBL Data Library, October 1992
A; Reference number: S33904
A; Accessions 30001 A; Molecule type: DNA
A; Residues: 2-330 <har></har>
A;Cross-references: EMBL:Z1730 B-makahachi w mada s c ohata w wikaido m wakai s c Hondo m
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference Influer: 33380/; MOLD:83801943 A;Accession: S33887
A; Molecule type: DNA
A; Residues: 88-113; 235-330 <tak></tak>
A;CrOss-references: EMBL:Z1/3/U Connavionam B a buttshansear H Gall W E Cortiliah D D Waxdal M.I * Edelma
Michaelistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seg
A. Contents: mveloma brotein Eu
A; Accession: B90563
 A; Molecule type: protein
 A; Note: this sequence has the Gim(3) marker, 97-Arg
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Blockmanistry 9, 317-3181, 1970 Blockmanistry 9, 317-3181, 1970 Brockmanistry 9, 317-3181, 1970
A; Reference number: A90564; MUID:71064025
A:Contents: Eu A:Accession: A90564
 A; Molecule type: protein
 A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2 A;Note: this sequence has the G1m(non-1) markers, 239-G1u and 241-Met
 R; Ponstingl, H; Hilschmann, M; 157 11604 1076
Hoppe-Seyler's Z. Physlot. Chem. 337, 1371-1004, 1370 A;Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Ni

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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u) with an IGHG4 conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
                                                                         Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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C.Date: 14 May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Date: 14 May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Date: 14 May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
R.Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A.; Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an SA; Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Gene: GDB:IGHG3
A;Genes: GDB:IB339; OMIM:147120
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14432.33-14432.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin c region; immunoglobulin homology
C;Seywords: immunoglobulin homology <IMM>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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82.8%; Pred. No. 2.8e-86;
tive 7; Mismatches 11
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Best Local Similarity
Matches 312; Conserv
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A; Residues: 1-377 <HUC>
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A/Gene: GDB:IGHG1
A/Map position: 14432.33-14432.33
A/Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin P;20 B$Cpomain: immunoglobulin homology <IM1>
F;243-310/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglob
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A91723
A; Accession: A91723
A; Molecule type: protein
B; Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Molecule to a moutation in disulfide bonds
A; Contents: annotation in disulfide bonds
A; Contents: annotation in Hischmann, N.
B; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
A; Title: Ruse of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID: 77070267
                                                                                                      A; Molecule type: protein
A; Residues: 1-34, Q', 36-96, KK, 98-115, Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A; Residues: 1-34, Q', 36-96, KK, 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
Note: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E; Jung, H.D.; Palm, W.; Hlaschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Prinamestruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 RA; Reference number: A91723; MUID: 83289131
A; Contents: myeloma protein KOL; disulfide bonds
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Pred. No. 4.5e-93;
3; Mismatches 0; Indels
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A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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Gramma-2a chain - 1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

Gracession: S37483

Area considered to the EMBL Data Library, February 1993

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 393
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                                                                                                        Length 377;
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                                                                                                                                                                                                                                                                                                             201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV-------
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                                                                                                     Score 1637.5; DB 2;
Pred. No. 3.7e-86;
7; Mismatches 11;
C;Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                        65.1%;
82.8%;
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Best Local Similarity 82.8
Matches 312; Conservative
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A; Molecule type: DNA
A; Residues: 1-326 < CELL>
A; Residues: 1-326 < CELL>
A; Cross-references: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A; Note: Lys-326 is probably removed posttranslationally
A; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A; Reference number: A92809; MUID: 81007873
A; Reference number: Myeloma protein Til
A; Accession: A92809
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A; Residues: 1-24, F., 75, 75-57, EV, 60-85;132-171, 222',175, 'B',177-193, 'D',195-196, 'Q', I A; Residues: 1-24, F.', 256-57, EV', 60-85;132-171, 222',175, 'B',177-193, 'D', 195-196, 'Q', I A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.W.
Mol. Immunol. 16, 923-925, 1979
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobul.
A; Reference number: A93132; MUID:80114419
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A; Residues: 1-19, '0', 21-57, '2', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Residues: 1-19, '0', 21-57, '2', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Rote: Trp-156 is at or near the complement-binding site
A; Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of Reference number: A90752; MUID: 80001357
A; Reference myeloma protein Zie
A; Accession: A90752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
R;Ellison, J: Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy of A;Reference number: A93906; MUID:82197621
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;rtitle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;rtitle: Disulphic My053; MUID:72033500
A;contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
RG-PTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQI
                                                                                                               KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                   NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                              359 ISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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A, Residues: 238-275 <HOF>
R, Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A, Reference number: A94591
A, Contents: annotation; Zie, revisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-2 chain C region - human
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A; Accession: A93132
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OMIM: 147130
A; Cross-references: GDB:119340;
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C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap thain disulfide bonds. In some cases, such as 194 and 194, the subunits associate into la C:Complex: An immunoglobulin c region; immunoglobulin homology civily. Immunoglobulin c region; immunoglobulin homology civily c:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology civily F:20-85/Domain: immunoglobulin homology civily. F:239-306/Domain: immunoglobulin homology civily. F:239-306/Domain: immunoglobulin homology civily. F:14/Disulfide bonds: interchain (to light chain) #status experimental F:14/Disulfide bonds: #status experimental F:27-83.140-200.246-304/Disulfide bonds: #status experimental F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Molecule type: DNA
A; Nesidues: 1-327 <ELL>
A; Note: the sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560
A; Accession: A90249
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C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 1
C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 1
C; Accession: A90933; A90249; A02150
R; Ellison, J.; Buxbaum, J.; Hood, L.
A) Mat, 11-18, 1981
A; Title: Nuclectide sequence of a human immunoglobulin C-gamma4 change and a human immunoglobulin C-gamma4 c
                             e.
                          A;Title: Structural studies of immunoglobulin A;Reference number: A93157; MUID:69064124 A;Contents: annotation; Sa, disulfide bonds
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                                                                                                                                                                                                          A; Cross-references: GDB:119338; OMIM:147110
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A; Residues: 1-30;81-326 <PIN>
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                                                                                                                                                                        A; Gene: GDB: IGHG2
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Best Local Simi
Matches 303;
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A; Map position: 14q32.33-14q32.33
A; Map position: 14q32.33-14q32.33
A; Introns: 99.1, 111/1, 221/1
A; Introns: 99.1, 111/1, 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C; Csuperfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin heterotetramer; immunoglobulin
F; 20-85, Domain: immunoglobulin homology <IM2>
F; 39-10/Region: hinge
F; 34-203, Domain: immunoglobulin homology <IM3>
F; 34-303, Domain: immu
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A; Residues: 138-161, 'L', 163-189,'FP', 193-474 < YAM>
A; Cross-references: GB:J00461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
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Pred. No. 4.5e-84;
9; Mismatches 15;
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Best Local Similarity 91.8%;
Matches 303; Conservative
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us-09-499-662-145.rpr

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C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: $40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, (... submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mab735 again A;Accession: $40295
A;Accession: $40295
A;Accession: 4446 <KLE>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Superfamily: immunoglobulin C region; immunoglobulin homology
C. Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
C. Superfamily: immunoglobulin c region cypoprotein; immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental cMAT>
F;1-117/Domain: V-D-J region cVHD>
F;118-446/Domain: C region cCHH>
F;118-214/Domain: C1 region cCH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region cCH2>
F;341-446/Domain: C3 region cCH2>
F;360-427/Domain: Immunoglobulin homology cIMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;224,227,229/Disulfide bonds: interchain (to lain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status experimental
                                                                             413
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  NQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
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                                                                                                                                                                                                                PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                       414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.4%; Score 1545; DB 2;
64.4%; Pred. No. 8.1e-81;
iive 59; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                              gamma-2a chain (mAb735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 WNSGSLSSSVHTLSQALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 1547; DB 1; Length 474; 61.2%; Pred. No. 6.7e-81; ive 67; Mismatches 108; Indels 1.
  untranslated
A; Title: Structure of the constant and 3' A; Reference number: A26235; MUID:80081501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 292; Conservative
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C; Accession: S22080; S06610; A31303
R; Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A; Reference number: S22080
A; Reference number: S22080
A; Residues: 1.470 <SAN>
A; Residues: 1.470 <SAN>
A; Residues: 1.470 <SAN>
A; Residues: 1.470 <SAN>
A; Cross references: EMBL: X62916; NID: 9439; PIDN: CAA44699.1; PID: 9440
R; Symons, D. B.A.; Clarkson, C.A.; Beale, D.
Rol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamme A; Reference number: S06610; MUID: 90097956
A; Accession: S06610
A; Molecule type: DNA
A; Residues: 142-470 <SEM>
A; Molecule type: DNA
A; Residues: 142-470 <SEM>
A; Molecule type: DNA
A; Residues: 142-470 <SEM>
A; Residues: 143-470 <SEM>
A; Residues: 15 CH gamma-1
A; Introns: 98/1; Ill/1; 221/1
C; Superfamily: immunoglobulin C region; immunoglobulin; membrane protein F; 161-225/Domain: immunoglobulin homology <IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 1476; DB 2; 60.4%; Pred. No. 7.2e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.4%
Matches 285; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
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                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S0131
A; Molecule type: mRNA
A; Residues: 1-475 CDEL3
A; Residues: 1-475 CDEL3
A; Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A; Note: this sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 V-GLLPFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 EEEMIKKQVILTCAVTDFAPDIXVEWINNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                              Ride Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, Bir. J. Balochen. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant imm A;Reference number: S01320; MUID:88329081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:119/Domain: signal sequence #status predicted <SIG>F:20-475/Product: Ig gamma-2b chain #status predicted <WAT>F:159-223/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66; Mismatches
                                                                                               438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Matches 289; Conservative
                                                                                                                                                                                                                          Ig gamma-2b chain precursor
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C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C. Accession: S69339; S72664
R. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A. Fittle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A. Reference number: S69339; MUID:95262687
A. Accession: S69339
A. Residues: 1-374 < KHA>
A. Reference number: S72664
A. Status: preliminary
A. Molecule type: mRNA
A. Status: preliminary
A. S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 NNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
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                                                                                                                                                                                                                                                                                                                                                                                               416 TIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                               114; Indels
                                                                                                                                                                                                                                                       Query Match 58.4%; Score 1469; DB 2; Best Local Similarity 59.6%; Pred. No. 1.8e-76; Matches 283; Conservative 66; Mismatches 114;
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochhan. Blophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porpoly, Reference number: JC5810; MUID:98063277
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A; Residues: 1-444 <AKA>
C; Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ap
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; 52.720, Domain: immunoglobulin homology x TMM>
F; 22.7Disulfide bonds: interchain (to 98) #status predicted
F; 99,7bisulfide bonds: interchain (to 109) #status predicted
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                                                                                                                                                                                                                                                                                        :|| |::| ::|| |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||| ||:|| ||:|||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
                                                                                                                                                                                                                                  5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVKQAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                        63 GLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARN-RDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 ALEWLALIFWDDD-KRYSPSLRTRLTITKDTSKNOVVLTMTNVDPADTATYYCGYSVEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
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                                       Length 374;
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                                            Score 1434; DB 2;
Pred. No. 1.4e-74;
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57.0%; Scor.
60.1%; Pred. No. 1...
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GOGYRFHSWGOGTLVTVSS--
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cDNA sequences of

5

9

Indels

Length 328;

260

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Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacskovics, I:;Sun, J:;Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence number: 147158; MUID:95015845
A;Accession: 147160
A;Accession: 147160
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Rolcule type: mRNA
A;Residues: 1-328 <RAC>
A;Cross_references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                    GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
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in: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                Query Match 50.1%; Score 1261; DB 2; Best Local Similarity 69.6%; Pred. No. 8e-65; Matches 231; Conservative 41; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
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C;Superfamily: imm
F;133-202/Domain:
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID:95015845
A; Accession: 147159
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
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7
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                    373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
                                                                                                   287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.3%; Score 1267; DB 2; 69.9%; Pred. No. 3.6e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                   434 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                    Mismatches
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Best Local S.
Matches 232
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August 14, 2002, 15:23:14; Search time 53.64 Seconds (without alignments) 339.265 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                OM protein - protein search, using sw model
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US-09-499-662-145 2517 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence: Scoring table:

105224 seqs, 38719550 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	no taita	Description	homo	homo	P01861 homo sapien	oryct		homo s	rattı	P22436 mus musculu	P01868 mus musculu	P20761 rattus norv	mns	P03987 mus musculu	P01863 mus musculu	P20762 rattus norv	P01864 mus musculu	P01865 mus musculu	ratt	P01866 mus musculu	P01867 mus musculu	Snw	mus	mus	mus	P01749 mus musculu	mus	P01753 mus musculu	P01748 mus musculu	P01855 rattus norv	28 mus m	P01854 homo sapien	29 mus п	1754 mus m	P23083 homo sapien
SUMMARIES	٤		GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC_RABIT	GC2_CAVPO	GC3_HUMAN	GC1_RAT	GC3_MOUSE	GC1_MOUSE	GCB_RAT	GC1M_MOUSE		GCAA_MOUSE	GCC_RAT	GCAB_MOUSE	GCAM_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	HV07_MOUSE	HV06_MOUSE	HV11_MOUSE	HV48_MOUSE	HV05_MOUSE	HV02_MOUSE	HV09_MOUSE	HV04_MOUSE	EPC_RAT	HV49_MOUSE		HV15_MOUSE	HV10_MOUSE	HV1G_HUMAN
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	Score		1758	1610	1599.5	1231.5	1210.5	1162	1155	1150	1145	1144.5	1140	1139	1129	1127.5	1126.5	1124	1115	1085	1080	560.5	526	522.5	522	514	208	203	489	486.5	486	486	481	480	477
	Result		1	7	m	4	2	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P06336 mus musculu P01743 homo sapien P01756 mus musculu P06329 mus musculu P06329 mus musculu P01747 mus musculu P01871 homo sapien P01871 homo sapien P01871 homo sapien P01873 mus musculu P01873 mus musculu P01873 mus musculu P01873 mus musculu
EPC_MOUSE HV1B_HUMAN HV12_MOUSE HV13_MOUSE HV03_MOUSE HV03_MOUSE HV03_MOUSE MUC_MOUSE MUC_HUMAN HV01_MOUSE MUC_ROUSE MUC_ROUSE
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421 1117 1117 1120 1120 1147 455 454 458
18.7 18.2 18.2 18.2 19.2 17.7 17.7 17.7 17.7 17.7
471 466 458 457 452.5 448.5 446.5 445.5 445.4 439 436.5
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## ALIGNMENTS

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PIB; PDB; IFC1; 15-JUL-92.

PDB; IFC2; 15-JUL-92.

MIM; 147100; ...

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003600; Ig_like.

Pfam; PF00047; Ig; 3.

SNART; SM00407; IG_like; 1.

SNART; SM00407; IGC1; 2.

PROSITE; PS00290; IG_MHC; 2.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                             99-177 AND 310-326 FROM N.A
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=72033500; PubMed-4940472;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S -> A (IN MYELOMA PROTEINS TIL & 21E).
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8310878C6878CF9C CRC64;
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91.8%; Pred. No. 1.8e-103;
iive 10; Mismatches 13;
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HINGE.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                         EMBL; J00230; AAB59393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 3. SMART; SM00410; IG_like; 1. SMART; SM00407; IGC1; 2. PROSITE; PS00290; IG_MHC; 2.
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haplotype.
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P01870;
                                        381
                                                                                                                                                                                                                                 TIDD RGC_RABIT
DDT 21-19
DDT 21-19
DDT 21-19
DDT 15-19
DDE 19 9
OCC MARMEDL
RRY BEEDL
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                                                                                                                                                                                                                                                                                        MEDLINE-70207560; PubMed-4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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INTERCHAIN (WITH A HEAVY CHAIN)
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35940 MW; 3EDBDB11EF208E7A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1599.5; DB 1
Pred. No. 9.5e-103;
9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K01316; AAB59394.1; ALT_INIT.
PIR; A02150; G4HU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like, 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 2.
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91.8%;
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                  Ig gamma-4 chain C region
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220
327
14
106
109
                                                      Homo sapiens (Human).
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MIM; 147130; -.
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27
106
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141
247
327 AA;
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                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     1:11-18(1981).
                                                                                                                   NCBI_TaxID=9606;
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DISULFID
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                                                                      MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region of the Fd sections of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostom1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 196: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA.
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"Sequence studies on the constant region of immunoglobulin G of different allotype.";
Biochem. J. 151:337-49(1975).
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                                                                                                                                                                                                                                          MEDLINE=70110015; PubMed=5461106;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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SEQUENCE FROM N.A.
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SEQUENCE OF 1-128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLSSVVSVTSSS---QPVTCNVAHPAINTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLFNGVRTFPSVRQSSGLY 63
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GC2_CAVPO

CC2_CAVPO

AC P01862;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

E 19 gamma-2 chain C region.

Cavia porcellus (Guinea pig).

CENKARYOTEN MELAZORA (Guinea pig).

CO EUKARYOTEN MELAZORA (Guinea pig).

CO EUKARYOTEN MELAZORA (Guinea pig).

CO Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                             48.9%; Score 1231.5; DB 1; Length 323; 70.0%; Pred. No. 1.6e-77; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
                                                                                    T -> M (IN D11 MARKER).

-> A (IN E15 MARKER).

-> E (IN REF. 2).

-> E (IN REF. 3).

-> E (IN REF. 3).

-> D (IN REF. 5).

      Immunoglobulin domain;
      Immunoglobulin C region.

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      NOR_TER
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      T -> M (IN D11 MARI VARIANT
      185

      185
      T -> A (IN E15 MARIANT

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SEQUENCE OF 4-68.
MEDLINE-71058471; PubMed-5538606;
                                                                                           HHZ>OZOZOWZWZZAZ
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            Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.9°
Best Local Similarity 70.0°
Matches 229; Conservative
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185
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1173
1187
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323 AA;
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 InterPro;
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### STRAIN OF STRAIN OF STRAIN OF STRAIN OF STRAIN OF STRAIN OF MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 MARED GUINEA PIGS.

13 MARED GUINEA PIGS.

HSSP, PO1772; 2FB4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003607; Ig_le1.

SMART; SM00410; Ig_like; 1.

SMART; SM00407; IG_12.

PROSITE; PS00299; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=71058474; PubMed=4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                       pig
the carboxyl-terminal
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Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5] SEQUENCE OF 227-311.
MEDLINE=75036073; Pubmed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-75036072; PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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CHAIN).
CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.1%; Score 1210.5; DB 1; Length 69.8%; Pred. No. 4.4e-76; Live 30; Mismatches 62; Indels
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                                                                                                                                                                                           Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-(f.2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                         [3]
SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; Pubmed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 13:4804-4811(1974)
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107
110
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142
178
248
329 AA;
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-!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CH1 REGION.
                                                       REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 435
                                                                    MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIOC. NAIL. ACAG. SCI. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE MENY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM MISCELLANEOUS: DISEASE PROTEIN OWN MAY REPRESENT AN ALLELIC FORM MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDEMVICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                           Frangione B., Rosenwasser E., Prelli F., Franklin B.C.; "Prinary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Blochemistry 19:4304-4308 [1980].
MEDLINE-82247835; PubMed-6808505; Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.; The amino acid sequence of 'heavy chain disease' protein 2UC. Structure of the Fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
                                                                                                                        290
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                                                                                                          DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-81021548; PubMed-6774747;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (DISEASE PROTEIN WIS)
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene deletion model.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                      GC3_HUMAN
ID GC3_HUMAN
AC P01860;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
DOMAIN 12 73 HINGE.
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S -> N (IN OMM).
/FTId=VAR_003894.
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/FTId=VAR_003891.
F -> Y (IN OMM).
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T -> A (IN OMM).
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11; Mismatches
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REMOVED PC
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PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 2.
SMART; SM00410; IG_Like; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
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MIM; 147120; -.
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                                                                                        GC1_RAT STANDARD; PRT; 326 AA.
P20759;
P20759;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Mamma-1 cregion.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                               Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 14:103-482(1988).
PIR: PS0017; PS0017.
PISSP: P01842; 7FAB.
INTEPPO: IPR003507; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
SMART; SM00407; IGcl; 2.
PROSITE; PS000290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GLYTLTSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG--GDCKPC----ICTG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 SEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE 173
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CHAIN).
                   CHAIN).
                                                                                                                                                                                                                                                                                                                                       region; Glycoprotein.
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63.4%; Pred. No. 2.8e-72;
tive 52; Mismatches 60;
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      CH1.

      CH2.
      CH2.

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176
326 AA;
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                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-89027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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; Pred. No. 6.2e-72;
44; Mismatches 68
                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region, secreted form.
Mus musculus (Mouse).
                                                                                                                                                  329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00451; -; NOT_ANNOTATED_CDS.
PIR; B02156; G3MSC.
HASSP; POL1857; 1FC1.
INTERPRO; 1PR003006; Ig_MHC.
INTERPRO; 1PR003597; Ig_C1.
INTERPRO; 1PR003597; Ig_C1.
INTERPRO; 1PR003500; Ig_like.
Ffan; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
IRMUNOGIODULIN GOMBIN; IMMUNOGIODULIN C:
IRMUNOGIODULIN GOMBIN; IMMUNOGIODULIN C:
ITANSMEMBYRANE; Alternative splicing.
294 EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK
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HINGE.
CH2.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity 65.09
Matches 215; Conservative
                                                                                                                                                  STANDARD;
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                                                                                                                                                  GC3_MOUSE
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ID GC3_M(
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GlycoSuiteDB; P01868; -.
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380 EMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 76-124 FROW N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Saldman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
              SEQUENCE FROM N.A.
MEDLINE-80045036; Pubmed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21). MEDILINE=80012837; PubMed-113776; ROGETS J., Clarke P., Salser W.; Sequence analysis of cloned cDNA encoding part of an ii.
                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Iff gamma-1 chain C region.
Mus musculus (Mouse).
                                                                                                                                            324 AA.
                                                                440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Nucleic Acids Res. 6:3305-3321(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine myeloma gammai chain.";
J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE-78242288; PubMed-98524;
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EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00795; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PIR; A02159; GIMS.
HSSP; P01842; 7FAB.
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                gamma 1 chain gene.";
Cell 18:559-568(1979)
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P01868;
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Ig gamma-2B chain c rey.co...
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
MGD; MGI: 56446; Igh.4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
SWART; SW0047; Ig. 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                LIGHT CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
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N -> D (IN REF. 3).

N -> D (IN REF. 3).

A338812F3D1F2C93 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Ig gamma-28 chain C region.
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SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
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276
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324 AA;
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es 207; Conserv
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P20761;
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Cell 18:559-568(1979).
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 3,
       "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
PIR; PS0018; PS0018.
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                                                                                                                                                                                                                                                                        MEDLINE-80045036; PubMed=115593; Honjo T., Cataoka T., Kawakami T., Takhashi N., Manno Y.; Takhashi N., Manno Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                          45.5%; Score 1144.5; DB 1; Length 333; 63.7%; Pred. No. 1.5e-71; ive 45; Mismatches 68; Indels 9;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                           INTERCHAIN (WITH A LIGHT CHAIN).
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                                                                                                         Immunoglobulin domain; Immunoglobulin C region.
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Il gamma-1 Chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                435 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                              HSSP; PO1842; 7FAB.

InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003609; Ig_lke.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC,; 2.
PROSITE; PS00290; IG_MHC; 1.
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333 AA;
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ID GCIM_MOUSE
AC P01869;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
**Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
**Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
**Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
**SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                        Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O. "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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Alternative splicing; Transmembrane.
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4CC88343B7A1CE27 CRC64;
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Pred. No. 3.7e-71;
5; Mismatches 60;
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CH2.
SEQUENCE OF 323-393 FROM N.A. MEDLINE=82197626; Pubmed=6804950;
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MGD; MGI:9646; 1Gh-4.
InterPro; 1PR003069; 1g_MHC.
InterPro; 1PR003597; 1g_C1.
Pfam; PF00047; 1g; 3.
SMARY; SM00407; 1GC1; 2.
PROSITE; PS00290; 1G_MHC; 1.
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Best Local Similarity 62.2<sup>3</sup>
Matches 206; Conservative
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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Matches
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                                                                                                                                                                                                        ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                         173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 232
                                                                                                                                                                                                                                                                                                                                                                                                                       201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                                                                                 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                             "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                            EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SEQUENCE FROM N.A.
MEDLINE-85027161; Pubwed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma - 3 chain C region, membrane-bound form.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 11:6775-6785(1983).
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
HSSP; P01857; IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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MEDILINE-81198976; PubMed=6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.", Nucleic Acids Res. 9:1365-1381(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                            Length 398;
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                                                                                                                                        (POTENTIAL).
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E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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                                                                                                                                                                                                                                                                          45.3%; Score 1139; DB 1;
64.7%; Pred. No. 4.5e-71;
11ve 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
19-VMX-2000 (Rel. 39, Last annotation update)
1g gamma-2A chain C region, A allele.
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POTENTIAL.
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HINGE.
Alternative splicing
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MEDLINE=81076554; Pubmed=6777755;
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les 213; Conservative
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1113
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3327
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363
333
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388
398 AA;
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SEQUENCE FROM N.A.
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    ransmembrane;
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MEDLINE-81223894; PubMed-6787604; ollo R., Auffray C., Morchamps C., Rougeon F.; demartson of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
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                                                                                                                                                                                          Bourgois A., Fougereau M., Rocca-Serra J.; "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
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                                                                                                                                                                                                                                                                                                                                                                                    "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
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B84361C5445A6864 CRC64;
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                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
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MEDLINE=74175517; PubMed=4831970;
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InterPro; 1PR003006; Ig_MHC.
InterPro; IPR003509; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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es 212;
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EEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                           141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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Sciurognathi; Muridae; Murinae; Rattus.
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Eur. J. Immunol. 18:317-319(1988).
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        Immunoglobulin domain;
        Immunoglobulin c region.

        NON_TER
        1

        DOMAIN
        97

        CH1.
        CH3.

        DOMAIN
        98

        114
        222

        CH2.
        CH2.

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15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
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                                                                                                                                     299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
                                                                                                         RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-88166903; PubMed-3127222;
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HSSP; P01857; 1FC1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003507; Ig_C1.
InterPro: IPR003507; Ig_like.
Pfam; PF00047; ig; 3.
SMART; $M00410; IG_like; 1.
SMART; $M00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rāttus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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143
249
329 AA;
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Thu Aug 15

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                              377
                                                                                                                                                                                                                                 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                               LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
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                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G gamma-2A chain C region, B allele.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6;
MEDLINE-82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreier P.H., Bothwell A.L.M., Mueller-eic acid sequences of the
Multiple differences between the nucleic acid sequences of the
IgGaaa and IgGaba alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 AA
                                                                                                                                                                                                                                                                                                                                                                                297 DSWARGDIYTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                              SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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SEQUENCE.
MEDLINE-82037777; PubMed-6794027;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SWART; SW0410; IG_like; 1.
SWART; SW0410; IG_like; 1.
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01, Last seq
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SEQUENCE FROM N.A.
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21-JUL-1986
15-JUL-1999
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|GLYTLSSSSYTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPHQRVPPCAA 119
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                                                                                                                                                                                                     REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
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                                           GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK----SCDKTHTCPPCPA
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Matches 207; Conservative
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## ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*

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Database

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*

SUMMARIES

DB

Query Match Length

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Description

Q9DBL4 Q99LC4 Q99L25 Q99L31 Q9R1A4 Q91Z05

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                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                :|::|:||:||:||:||:||| DVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K - - - - - SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 IEKTISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                      DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (REB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (REB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003451; AAH03435.1; -. HSSP; P01842; 7FAB. InterPro; PRR003599; 1g.cl. InterPro; IPR0035097; 1g.cl. InterPro; IPR003600; 1g_like.
                                                                                                                                                                                                                                                         9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                    65.1%; Score 1637.5; DB 13
63.7%; Pred. No. 1.9e-129;
ive 70; Mismatches 94;
             InterPro; IPR003599; Iq.
InterPro; IPR003599; Iq.
InterPro; IPR003509; Ig_c1.
InterPro; IPR003006; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PR00047; Ig; 4.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 1.
SWART; SW00410; IG_like; 1.
PROSITE; PS00290; IG JHC; UNKNOWN_1.
SRQUENCE 473 AA; 51699 MW; 9DED57A
                                                                                                                                                                                                                                                                                                                                                              Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                      Query Match
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099LC4;
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61 GQGLEWYGEIYPGSGNTYYSEKFKGKATLITDKSSSTAYMILSSLTSEDSAVYFCARSSY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 RDCG----CKPCICTVPEV---SSVFIEPPKFKDVLTITLTPKVTCVVVDISKDDPEVQF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                      Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
HSSP; P01842; FFAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 3.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_Like; 1.
PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SROUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                      DB 11;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                64.6%; Score 1626.5; DB 11
63.6%; Pred. No. 1.5e-128;
ive 72; Mismatches 89;
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MRC.
Interpro; IPR003596; Ig_W.
Pfam; PF00047; ig; 4.
SMART; SM004409; IG; 2.
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07:56:12

Thu Aug 15

96352328B3332ADB CRC64;

51661 MW;

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SEQUENCE
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                                                                                                                                                                                  121 --YSNN-WYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                        TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                              VEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                    VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
                                                                                                                                                                                                                                                                                                               EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
                                                                                       Gaps
                                                                                                                  1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             473;
                                                                  63.0%; Score 1586.5; DB 11; Length 63.4%; Pred. No. 3.7e-125; ive 61; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0995131;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00407; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                            Similarity
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                                                                  Ouery Match
Best Local S
Matches 301
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Mide K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (MaD 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; -..
INTERFO: IPR003006; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003596; Ig_W.C.
InterPro; IPR003596; Ig_V.
SWART; SM00401; IG_like: 2.
                                                                                                                                                                    416
                                     Gaps
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                                                                    YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                  181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                     241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
62.1%; Score 1564; DB 11; ilarity 63.1%; Pred. No. 2.8e-123; Conservative 60; Mismatches 108;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
GAWMA1 HEAVY CHAIN OF MAB7 (FRAGMENT)
Mus musculus (Mouse).
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 Query Match
Best Local Similarity
Matches 298; Conserv
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Q9R1A4;
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                                                                                                                             60 DSVKGRETIYKDKDRNILSLQMSSLRSEDTAMYYCARG-DYS----AYWGPGTLVTVSA 113
                                                                                                                                                                   ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                      379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                            67 MGEIDPSDSYTNYNOKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 184
                                                                                   5
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                                                                                                                                                                                                                        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
                                                       21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQGLEWMGEIDPSDSYTNYN
                                                                      259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
  DB 11; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 1422.5; DB 11; Lengtl
57.1%; Pred. No. 2.3e-111;
ive 74; Mismatches 114; Indels
                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ database:
EMBL; BCO103277, AAH10327.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91205 PRELIMINARY; PRT; 473 AA.
Q91205;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                             96;
57.0%; Score 1435.5; DB 1
59.3%; Pred. No. 1.7e-112;
ive 71; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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              Similarity
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Query Match
Best Local S:
Matches 268
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Matches
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"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998). EMBL: AJ300675; CAC44624.1; -...
                                                                                                                                             ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
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                            :|:|||||||:|||||||::|| ||||||::|| SLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPI
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                                                                                                                                                                                                                                         298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Last sequence update)
Last annotation update)
CHAIN CONSTANT REGION
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Wagner B., Overesch G., Sheoran A., Holmes
Leibold W., Radbruch A.;
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Length 278;

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Query Match 36.9%
Best Local Similarity 36.7%
Matches 212; Conservative
                         Conservative
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             Similarity
             Best Local Sin
Matches 186;
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                          Huzz., Garen A.;
"Targeting tissue factor on tumor vascular endothelial cells ar cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AAK58686.1; -. SEOUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
SUBMITTED (AUG-2007; AAH12207.1; -.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                            096P08.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0921K1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
                                                     LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                       701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE-21477448; PubMed-11593034;
                                                                                                                                                                                                                                                                                                                                                             al Similarity 99.1%;
230; Conservative
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                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local
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                                                                                                                                                         YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GQALEWMGWITPFNGNTNYAQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YSNNW--YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPD 357
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CDKTHTCP----
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. SEEF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.9%; Score 929.5; DB 4;
36.7%; Pred. No. 1.1e-69;
iive 84; Mismatches 166;
Score 984; DB 11;
Pred. No. 8.8e-75;
; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                    241 K----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
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  39.1%; Scc
67.1%; Pre
tive 33;
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01-DEC-2001 (TrEMBLrel. 19, Las:
01-DEC-2001 (TrEMBLrel. 19, Las:
UNKNOWN (PROTEIN FOR MGC:15420)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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us-09-499-662-145.rspt

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NCBI_TaxID=9606;
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SEQUENCE 50
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462 GK
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----VELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                          358 QDTAIRVFAIPPS-FASIFLTKSTKLTCLVJDLTTYD-SVTISWTRQNGEAVKTHTNISE
                                                                                  EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                        376 PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011488; AAH13488.1;
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          091WT3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.0 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                      431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
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263
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121 SYSSCQNDYXYXYMDVWGKGTTVTVSSASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPSQDVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYS---NNWYF----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEP
                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HYMO Sapiens (Human).
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.0%; Score 857; DB 4; Lv 40.9%; Pred. No. 9.9e-64; Live 69; Mismatches 177;
                                                                                                                                                                                                                                             Ą.
                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00409; IG; 4.
SMART; SM00409; IG: 2.
SMART; SM00406; ICV; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF00047; Ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-PROSTATE;
Strausberg R.;
Submitted (APR-2001) to the EM
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.0
Best Local Similarity 40.9
Matches 205; Conservative
                                                                                                                                                                                                                                             PRELIMINARY;
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500 AA; 5
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18;

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Q91WR1;
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Q96BB9
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            Q91WR1
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 Q91WR1
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             61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 NCPGICSPPTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
                                                                                                                                                                                                                                                                                                                                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                             091WT1 PRELIMINARY; PRT; 481 AA.
091WT1;
091WT1;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
HYBOTHETICAL 52.1 KDA PROTEIN.
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                       Length 481;
                                                                                                                                                                                                                                                                                                                                     33.2%; Score 834.5; DB 11; Length 40.2%; Pred. No. 7.4e-62; ive 73; Mismatches 184; Indels
                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
Hypothetical protein.
SEQUENCE 481 AA; S2105 MW; 97DF68D159463F65 CRC64;
                                         VMHEALHNHYTQKSLSLSPGK 470
                                                      ll protein,
481 AA; 52105 MW;
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.2%
Matches 194; Conservative
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
GK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GK 470
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                              RESULT 13
Q91WT1
ID Q91WT1
                                                               462
395
                                         450
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GOGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 -PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096BB9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 818; DB 11; Length 41; Pred. No. 1.8e-60; 85; Mismatches 177; Indels
                                                                                                                                                                                                                           TISSUE=KIDNEY;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC013539; AAH13539.1; -.
Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64:
                                                                                                                                                                                                                                                                                                                     al protein.
488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                        Last sequence update)
Last annotation update)
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                                       Created)
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                                   01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 53.0 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                   32.5%;
39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 LSLSPGK 470
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464 IDRLSGK 470
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Best Local Simi
Matches 191;
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16;

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18;
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                                                                                                                                                                                                                                                                                                                                        DYSNNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                            176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLEWMGEIDPSDSYTNYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYYCARN-R 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF 428
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                         300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 N-----TKVDKRVEPKS-----CDKTHTCP-----
                                                                                                                                                                   Query Match 32.4%; Score 814.5; DB 4; Length 597; Best Local Similarity 32.6%; Pred. No. 4.8e-60; Matches 190; Conservative 94; Mismatches 179; Indels 119;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
                                         SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 -----PCPAPELLGGPS-
                                                                                                                                                                                                                                                                                                                                        120
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Search completed: August 14, 2002, 15:22:18 Job time: 686 sec

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August 14, 2002, 15:15:38; Search time 230.21 Seconds (without alignments) 226.770 Million cell updates/sec
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Compugen Ltd.
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                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
 GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2517
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length: 2000000000
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Perfect score:
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Maximum DB s
                                                               OM protein
                                                                                                                                                                                                    Sequence:
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1: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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4: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
5: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
5: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
6: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
7: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
8: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
9: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
11: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
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22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:* 14: 15: 17: 19: ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Humanised HFE7A de	Humanised HMFG-1 h
SUMMARIES			ID	_	AAW90933	AAW90934	AAW83037	AAB14779	AAW90929	AAW83036	AAB14776	AAW90926	AAW90936	AAM52156
		;	DB:	21	21	21	19	21	21	19	21	21	21	22
			Match Length DB ]	470	470	470	470	470	470	470	470	470	470	731
	dФ	Query	Match	100.0	66.66	8.66	99.8	8.66	8.66	99.2	99.2	99.5	99.2	93.3
		,	Score	2517	2514	2512	2511	2511	2511	2498	2498	2498	2498	2349.5
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(SANY ) SANKYO CO LTD.

Humanised HMFG-1 h	Humanised HMFG-1 h	HMFG-	Humanised HMFG-1 h	Humanised HMFG-1 h	Heavy chain of hmA				Chimeric 2403 IgG	Monoclonal antibod	Sequence of antibo	Human reshaped F19	Completely humanis	Amino acid sequenc	Antibody D heavy c	Ganglioside GM2 an	Human immune syste	Recombinant 1mmuno	Humanised anti-IL-	Humanised anti-IL-	Chimeric mouse/hum	Anti-IL-8 humanise	Human type antihum	Amino acid sequenc		Pe P	Anti-5T4 single ch	Amino acid sequenc	Human type antihum	type	D9D10 heavy chain	MoTAbil fusion pro	Reshaped CAMPATH-1
AAM52159	AAM52158	AAM52161	AAM52157	AAM52160	AAW48650	AAB72228	AAB72232	N	AAE03755	ø	AAR24442	AAY50166	AAR43339	AAW49816	AAR31023	AAB83156	AAB36210	AAY29458	AAB30322	AAY77766	AAY50157	AAW69316	AAG64475	AAB83838	AAU14177	AAG64471	AAW86003	64	AAG64469		AAW85689	σ	AAR22757
22	22	22	22	22	19	22	22	21	22	20	13	20	14	19	14	22	22	20	21	21	20	19	22	22	22	22	20	22	22	22	20	20	13
741	729	739	730	740	652	465	464	470	466	476	481	472	449	449	476	583	467	452	452	452	472	452	473	592	474	473	595	475	473	473	468	711	470
93.3	93.1	93.1	92.9	92.9	91.7	91.1	6.06	7.06	7.06	89.7	9.68	89.4	88.8	88.8	88.7	88.5	87.6	87.5	87.5	87.5	87.5	87.2	87.1	87.0	87.0	6.98	6.98	86.8	86.8	86.5	86.4	86.4	86.0
2349.5	2344.5	2344.5	2338.5	2338.5	2307	2293.5	2288.5	2284	2283	2258	2254.5	2251	2235	2235	2233	2226.5	2205.5	2203.5	2203.5	2203.5	2203	2194.5	2191.5	2190	2189	2188.5	2187	2184.5	2183.5	2176.5	2174	2174	2165
12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; mysthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpure; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed heavy chain Heu 3 protein. AAW90935 standard; Protein; 470 AA 98JP-0276881. 98JP-0276882. 99EP-0307711. 08-AUG-2000 (first entry) 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; 05-APR-2000. EP990663-A2 Synthetic. AAW90935; AAW90935 

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ilgand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-anemic, anti-anemic, anti-architic, anti-irral, immunomedulatory, dermatological, immunosuppressive, thyromimetic, anti-arteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, remunatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autolumune hemolytic anemia, sterility, mysathenia gravis, multiple sclerosis, Basedow's disease, thromboodpara insulin and anomaly disease. dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mind the native ligand, do not induce liver disease, and have reduced risk of a human anti-nurine antibody response. This sequence represents which is described in the method of the invention. New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems Tamaki I, Takahashi T; Nakahara K, 2; Page 180-182; 263pp; English. Haruyama H, WPI; 2000-258930/23. N-PSDB; AAA11646 Serizawa N, Claim 

470 AA; Sequence

ö 240 300 420 GOGLEWMGEIDPSDSYTNYNOKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 Gaps 9 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS ö Length 470; Indels DB 21; 100.0%; Score 2517; DB 21; 100.0%; Pred. No. 1.7e-144; ive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 470; Conservative 61 61 121 181 241 241 121 181 301 301 361 ò 셤 ò 셤 ò g ò qq ă g ò g å

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosotlerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimcto disease; rheumatoid arthritis; graft versus host disease; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. 361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420 Takahashi T; 421 ldsdgsfflyskltvdksrwqqqnvfscsvmhealhnhytqkslslspgk 421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK Humanised anti-Fas designed heavy chain Heu 1 protein. Serizawa N, Haruyama H, Nakahara K, Tamaki I, AAW90933 standard; Protein; 470 AA. 99EP-0307711. 98JP-0276881. 98JP-0276882. 08-AUG-2000 (first entry) (SANY ) SANKYO CO LTD. WPI; 2000-258930/23. N-PSDB; AAA11644 29-SEP-1999; 30-SEP-1998; 30-SEP-1998; 05-APR-2000. EP990663-A2 Synthetic. AAW90933; N AAW90933 RESULT ò g 

Interpretation describes a mover interpretation to the cells with an abnormal Fas/Fas incledie (1) that, induces a poptosis in cells with an abnormal Fas/Fas concleded to the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between cardiats ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antinfertility, neuroprotective, antitarteriosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of Ilgand binding. (1) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft active shost disease, solecterms syndrome, pernicious or hypoplastic anemia, Addison's disease, solecterm, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura insulin cardiomyopathy, glomerulomophitis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (1) selectively This invention describes a novel humanized anti-Fas antibody-like

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

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inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-nurine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu I which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-alleggic, anti-arthritic, antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; mephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                 Score 2514; DB 21;
Pred. No. 2.6e-144;
1; Mismatches 0;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between comportations in cells with a normal system, by inhibiting binding between the products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, antiranemic, nephrotropic, anti-allergic, anti-arthritic, antiviral, antirheumatic, nephrotropic, antimerallity, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce completion of ligand binding. (I) are used to treat and/or prevent disease associated with the Fas/Fas ligand system, especially systemic unbibition of ligand binding. (I) are used to treat and/or prevent disease, Sjorgen's syndrome, pernicious or hypoplastic complay host disease, soleroderma, Goodpasture syndrome, Composition of disease, slorgen's syndrome, pernicious or hypoplastic anemia, attentity, myasthenia gravis, conditionyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectives; so can be evaluated in colls. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents con humanised anti-Fas antibody heavy chain construct designated Heu 2 was a humanised anti-Fas antibody beavy chain construct designated Heu 2 was an expectable of the nethod of the invention.
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Pred. No. 3.5e-144;
                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces
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                                                                                                                                                                                                                                                                                                                                   cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                        Claim 2 ; Page 174-176; 263pp; English.
                                                                                                                                                                                               Nakahara K,
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                                                       99EP-0307711
                                                                                          98JP-0276881
98JP-0276882
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                                                                                                                                                      (SANY ) SANKYO CO LTD.
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EP990663-A2

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Masahiko O,
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                                                              YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                     361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                     HFETA; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; systemic lupus erythematosus; graft versus host disease; stofacderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthania gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteniosclerosis; myocarditis; cardiomyopathy; glomerular nephirtis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                     LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                             Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
                                                                                                                                                                                       Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                 1..19
/label- Sig_peptide
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20..140
/label- Variable
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                                                                                                                                         AAW83037 standard; Protein; 470 AA
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118.129
/label= CDR_H3
/note= "claim 9"
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/label- Constant
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/label= CDR_H1
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/label= CDR_H2
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97JP-0082953
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                                                                                                                                                                                                                                                                                                   Homo sapiens.
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01-APR-1997;
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This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. It includes humanising R4d6 and A76T amino acid substitutions that are are conserved in the human IGG heavy chain. Host Escherichia coli pathoHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion fragment of the humanised HV type HFE7A heavy chain and DNA cancoding human IGG1 constant region (see AAAVO080), and is deposited as FERM BP-6273 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW8301-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, solorens anomalia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thermatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thermatoid arthritis, myocarditis, cardiomyopathy, glomerulain nephritis, hypoplastic myocarditis, cardiomyopathy, glomerulain repection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                      antibodies and proteins bind conserved epitope of Fas antigen - 1 to evaluate drugs in animal models and to treat Fas-associated bases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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99.6%; Pred. No. 4e-144;
Live 2; Mismatches 0;
Tohru T;
                                                                                                                                                                                                                                                                                                                        Claim 22; Page 225-227; 292pp; English.
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diseases e.g. autoimmune disease,
myocarditis, hepatitis and AIDS
Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.6
Matches 468; Conservative
Nobufusa S,
                                                            WPI; 1998-543440/47.
N-PSDB; AAV70080.
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98JP-0276882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allowerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                     Anti-Fas antibody, monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Iigand, apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                            an abnormality contains
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421 ldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                           wentive or treating agent for the diseases caused by the Fas/Fas ligand system e.g. autoimmune diseases, c
                                                                                                                                Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
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Pred. No. 4e-144;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 108-109; 139pp; Japanese.
                                                          AAB14779 standard; Protein; 470 AA
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                                                                                                         (first entry)
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Chimeric - Homo sapiens.
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Best Local Similarity
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinherility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Godpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                   YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
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capoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, anti-allergic, anti-arthritic, antivaral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antintreniscientic, cardiant and hepatropic activity. (I) induce antiarterisoclerotic, cardiant and hepatropic activity. (I) induce antiarterisoclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capptosis assesses associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis; graft versus host disease, Slorgen's syndrome, permittions or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cardiomyopathy, glomerulonephritis, hepatis; (fulminant, chronic, viral cappetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatis; (fulminant, chronic, viral cardiomyopathy, glomerulonephritis, hepatis; (fulminant, chronic, viral calls. They bind to both human and murine Fas, so can be evaluated in mumulised anti-Fas antibody HEP7A designed heavy chain which is used in the method described in the invention.
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470 AA; Sequence

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                                                                                                   GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                  WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                      241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                          361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                          Gaps
                                                  1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
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Score 2511; DB 21; Length 470;
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                       Indels
           Pred. No. 4e-144;
2; Mismatches 0;
99.88;
99.68;
                       Conservative
           Local Similarity
           Best Local Simi
Matches 468;
Query Match
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HFE7A, monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A, autolimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune hemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease;
                                                                             thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                     Location/Qualifiers
1..19
1..19
20..470
/label= Mat_protein
                                                                                                                                                                                                20..140
/label= Variable
                                                                                                                                                                                                                   141..464
/label- Constant
                                                                                                                                                                                                                                                        'note= "claim 9"
                                                                                                                                                                                                                                                                                  "claim 9"
                                                                                                                                                                                                                                                                                                     /label= CDR_H3
/note= "claim 9"
                                                                                                                                                                                                                                                                 69..84
/label= CDR H2
                                                                                                                                                                                                                                       50..54
/label= CDR_H1
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97JP-0169088.
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                                                                                                                              Homo sapiens.
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25-JUN-1997;
                                                                                                                                                                                                                                                                                                                               AU9859701-A.
                                                                                                                                                                                                                                                                                                                                                 08-OCT-1998
                                                                                                                                      Synthetic.
                                                                                                                                                                Peptide
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This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. colipgHSL7A62 SARK 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human IgGl constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised of inducing apoptosis in abnormal cells expressing Fas, and of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to antibodies and proteins bind conserved epitope of Fas antigen - 1 to evaluate drugs in animal models and to treat Fas-associated masses e.g. autoimmune disease, allergy, atopy, arteriosclerosis, Claim 22; Page 212-213; 292pp; English. used to evaluate drugs in animal m diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS WPI; 1998-543440/47. N-PSDB; AAV70079. New

AAW83036 standard; Protein; 470

AAW83036

(first entry)

15-MAR-1999

AAW83036;

XXXXXX

Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I; Masahiko O, Nobufusa S, Shin Y, Tohru T;

us-09-499-662-147.rag

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30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Iigand; apoptosis modulator; programmed cell death; autolimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia. Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosolerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                Gaps
                                                                                                                                                                                              1 MCWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-Fas antibody heavy chain, SEQ ID NO:89
                                                                                                                                        99.2%; Score 2498; DB 19;
99.1%; Pred. No. 2.5e-143;
ive 2; Mismatches 2;
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                                                                                                                                                               Conservative
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    Homo sapiens.

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466; Conserv
                                                                                                         470 AA;
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HEFTA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HEFTA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autofinance diseases, allery, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS represent the heavy chains (or fragments thereof) of various humanised HFETA-derived anti-Fas antibodies.
                                                                                                                                                                                                                                for the diseases caused by an abnormality
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Pred. No. 2.5e-143;
;; Mismatches 2;
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                                                                                                                                                                                                                                Preventive or treating agent
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99.1%;
99JP-0278301.
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                                                                                                    (SANY ) SANKYO
                                                30-SEP-1998;
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Matches 466;
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AAW90926 standard; Protein; 470 AA.

AAW90926;

(first entry) 08-AUG-2000

Humanised HFE7A designed heavy chain protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; albergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2

05-APR-2000.

99EP-0307711 29-SEP-1999; 98JP-0276881 30-SEP-1998;

98JP-0276882. 30-SEP-1998;

(SANY ) SANKYO CO LTD.

Nakahara K, Tamaki I, Takahashi T; Serizawa N, Haruyama H,

WPI; 2000-258930/23. N-PSDB; AAA11597 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 15; Page 134-136; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cell surface, and prevents

apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,

anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antiarteriosolerotic, cardiant and hepatropic activity. (I) induce

antiarteriosolerotic, cardiant and hepatropic activity (I) induce

thibitition of ligand binding (I) are used to treat and/or prevent

clupus extythematosus, Hashimuco disease, rheumatoid arthritis, graft

versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

clasease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosolerosis, myocarditis,

cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejectively induce it in abnormal

cells. They bind to both human and murine Fas, so can be evaluated in

murine disease models: (I) act on the active site of Fas, i.e. they mimic

the native ligand, do not induce liver disease, and have reduced risk of

a humanised anti-maine antibody response. This sequence represents

a humanised anti-maine antibody response. This sequence represents

the partorice and pres

AA; 470 Sequence

the method described in the invention.

CO LTD.

(SANY ) SANKYO

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                                                                                                                                                                                                                                                                                                                 300
                                                                                                                           61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                             121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                 Gaps
                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                                                          361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv
                                                                                                                                                                                                                                                                                                                 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KAKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                    181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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Length 470;
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                                 Indels
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   DB 21;
   Score 2498; DB 21;
Pred. No. 2.5e-143;
                                 2; Mismatches
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   99.2%;
99.1%;
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                                    Conservative
 Query Match
Best Local Similarity
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                                 Matches 466;
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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
cappotosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyronimetic,
antirheumatic, nephrotropic, antimifertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity (I) induce
continues by binding to cell surface Fas or inhibit it by competitive
continues by the man to cell surface Fas or inhibit it by competitive
continues binding. (I) are used to treat and/or prevent
continues associated with the Fas/Fas ligand system, especially systemic
colliseases associated with the Fas/Fas ligand system, especially systemic
collisease, soloroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
cells and inhebetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells and humanised anti-murine antibody response. This sequence represents
con human anti-musine antibody response. This sequence represents
con human anti-musine antibody response. This sequence represents
con human anti-musine antibody response.
                                                                                                                                                                humanized anti-Fas antibody, useful for treating or preventing e.g. Lammatory or autoinmune disease, induces apoptosis selectively in
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                             Takahashi
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                             Tamaki I,
                                                                                                                                                                                                                         cells with abnormal Fas-Fas ligand systems
                             Х,
                                                                                                                                                                                                                                                                                 Claim 2; Page 188-189; 263pp; English.
                             Nakahara
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470 AA; Sequence

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                                                                                       GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                        KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                       Gaps
                                                                 9
                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                        WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                        YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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   Length 470;
                       Indels
  DB 21;
 Score 2498; DB 21;
Pred. No. 2.5e-143;
                      3; Mismatches
99.2%;
98.9%;
          Best Local Similarity 98.9
Matches 465; Conservative
  Query Match
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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-268 and encoded by ABA02682-ABA02128. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                         Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; portion
for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity f polymorphic epithelial mucin, and cytotoxic portion having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
             421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                             Humanised HMFG-1 heavy chain/DNase I fusion protein
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Pred. No. 3.8e-134;
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                                                                                            AAM52156 standard; Protein; 731
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                                                                                                                                                                                                                      cytotoxic; endonuclease; DNase
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                                                                                                                                                                                                                                                                                                                                                                        03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    (ANTI-) ANTISOMA RES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                         AAM52156;
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MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytocoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                          Humanised monoclonal antibody; polymorphic epithelial mucin; PEMI;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
              237
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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                       KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                       LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                    Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
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                                                                                                                                                                                                                                                                          AAM52159 standard; Protein; 741
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02-OCT-2000; 2000US-237159P
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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nonoclonal antibody; polymorphic epithelial mucin; PEM1; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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for
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                                         YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                              GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                            KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                  LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised monoclonal antibody;
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Length 741;

DB 22; 10;

93.3%; Score 2349.5; DB 2; 93.2%; Pred. No. 3.8e-134; ive 19; Mismatches 10;

al Similarity 93.2 438; Conservative

Query Match Local

Best Loca Matches

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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                  121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                     KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                           DB 22; Length 729;
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                                                                                                                                  Indels
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                                                                                                                                  10;
                                                                                                        93.1%; Score 2344.5; DB 2:93.2%; Pred. No. 7.5e-134; ive 19; Mismatches 10;
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                                                                                                                   Local Similarity 93.2 nes 437; Conservative
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cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                               Novel compound used to treat cancer has target cell-specific comprising humanised monoclonal antibody having specificity follymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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Pred. No. 7.6e-134;
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93.2%; Pred. No. 1.7e-133;
tive 19; Mismatches 10;
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2000US-237159P
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                                                                                                                                               LTD.
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Best Local Similarity 93.2
Matches 436; Conservative
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Search completed: August 14, 2002, 15:15:40 Job time: 838 sec

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Sequence 17, 18 Sequence 17, 18 Sequence 12, 18 Sequence 9, 18 Sequence 9, 18 Sequence 5, 18 Sequence 5, 18 Sequence 12, 18 Sequence 2, 18 Sequence 2, 18

81,

Sequence Sequence Sequence Sequence 7 Sequence 7 Sequence 8

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Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: TSO, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.8%; Score 2235; DB 1;
93.3%; Pred. No. 6.6e-159;
live 13; Mismatches 15;
US-09-679-397-2
US-07-934-3736-23
US-08-437-642B-23
US-08-447-55-3
US-08-447-55-3
US-08-157-101A-7
US-08-704-744-81
US-08-049-672A-4
US-08-049-672A-4
US-08-337-11-7
US-08-337-11-7
US-08-487-550-12
US-08-487-550-4
US-08-461-9688-5
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 13:
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MEDIUM TYPE: Floppy disk
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     STRANDEDNESS: single
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CITY: San Francisco
STATE: California
COUNTRY: USA
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2517
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
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1: /cgn2_6/ptodate/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodate/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcyrG_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcyrG_COMB.pep:*
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Compugen Ltd
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US-09-049-672A-8
US-09-02-449-71
US-09-485-737B-67
US-09-485-737B-90
US-09-485-737B-90
US-09-437-642B-22
PCT-US93-07832-22
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US-08-887-352B-14
US-08-887-352B-16
US-09-109-207C-14
US-09-109-207C-16
US-09-296-005-16
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US-09-109-207C-18
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US-09-054-255-2
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
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                                                                                                                                                                                                                                                                         140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY
                                      1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
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Patent No. 5876961
GENERAL INFORMATION.
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
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N.W.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILLING DATE: 01-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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TOPOLOGY:
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US-08-378-939-10
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61 GQGLEWMGGIPLEGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDRY 120
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                                                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: You, Henry
APPLICANT: Quegler, Weil C.
APPLICANT: Baughn, Mariah R.
TILE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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                                                                                                                Indels
                                                                   88.7%; Score 2225;
88.7%; Pred. No. 1e-158;
+ive 20; Mismatches 28;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09049672A Patent No. 6135941
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IBM Compatible
                                                                                              Best Local Similarity 88.7 Matches 422; Conservative
protein
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MEDIUM TYPE: Diskett
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 MOLECULE TYPE:
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     US-08-378-939-10
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US-09-049-672A-8
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                                                                             Query Match
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COMPUTER READBALE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC Comparatible OPERATING SYSTEM: PC Comparatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,449 FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 91085R3-2
TELECHONE: 650/225-5530
TELECHONE: 650/225-5530
TELECHONE: 650/225-5530
TELECHONE: 650/225-5530
TELECHON FOR SEQ ID NO: 71:
SEQUENCE CHARRACTERISTICS:
TENDORMATION FOR SEQ ID NO: 71:
 South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 452 amino acids TYPE: Amino Acid
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                  California
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US-09-026-985-71
                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 MGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 426
                                                                                                                                                                                                                                                                                                                                                                                                                           7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Dresta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                                                                                                                                                                                                                                                                                           87.6%; Score 2205.5; DB 4
89.4%; Pred. No. 1.1e-156;
iive 18; Mismatches 28;
                                                           39,132
R: PF-0497
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Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
                                         NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Genentech, Inc.
1 DNA:Way
             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 89.4 Matches 415; Conservative
                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                             ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
APPLICATION NUMBER:
                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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                                                                                                                                       TELEX:
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80 NOKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGTLVIV 138
                                                                                                                                                                                         SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                 Gaps
                                                              20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                           9
                                                                                 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                     GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
 Length 452;
                               17; Indels
 DB 3;
                   Pred. No. 1.5e-156;
87.5%; Score 2203.5;
90.3%; Pred. No. 1.5e
live 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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APPLICANT: Sablon, Erwin TTLE OF INVENTION: INTERPRENON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK, TITLE OF INVENTION: INTERPRENON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK, TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS FILE REFERENCE: INNS:015
CURRENT PAPELCATION NUMBER: US/09/485,737B
CURRENT PAPELCATION NUMBER: P8/05165
PRIOR PLILING DATE: 1998-06-14
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PALENT VALUE OF SEQ ID NOS: 104
SSEQ ID NO 67
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 THICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 86.4%; Score 2174; DB 4; Best Local Similarity 88.0%; Pred. No. 2.5e-154; Matches 409; Conservative 21; Mismatches 31;
   421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
                                                                                                         Sequence 67, Application US/09485737B Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 90, Application US/09485737B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: SYNTHETIC US-09-485-7378-67
                                                                                                                                                              APPLICANT: Buyse, Marie-Ange APPLICANT: Sablon, Erwin
                                                                                                                                            GENERAL INFORMATION:
                                                                                        US-09-485-737B-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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                                                   APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.5%; Score 2203.5; DB 4; Best Local Similarity 90.3%; Pred. No. 1.5e-156; Matches 408; Conservative 26; Mismatches 17;
                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/POCKET NUMBER: 91085R3-1
TELEPHONE: 650/225-530
TELEPHONE: 650/225-530
TELEFAX: 650/25-530
TELEFAX: 650/352-9881
INFORMATION FOR SEO ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
Sequence 71, Application US/09026985 Patent No. 6133426 GENERAL INFORMATION:
                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                               Genentech, Inc
                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                               ADDRESSEE:
STREET: 1
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Gaps

4;

Length 468; Indels 185

302 365 disk

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LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 NQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGQGTLV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQQSGPELVKPGASVKISCKTSCYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2158.5; DB 2
Pred. No. 3.4e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                     E: 3.5 inch, 1.44 Mb floppy
IBM PC compatible
                                                                                                                                                                        SOFTWARE: Winderin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     P0709P2
                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                CITY: South San Francisco
STATE: California
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89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 454 amino acids TYPE: Amino Acid
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                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee, Wendy M.
                  DNA Way
                                                                                                                                                            OPERATING SYSTEM:
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Best Local Similarity
ADDRESSEE:
STREET: 1
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                                                                                                                                               COMPUTER:
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                                                                       COUNTRY:
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                            APPLICANT: BUYSE, Marie-Ange
APPLICANT: BASE, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISBASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
FILE REFERENCE: 1000-02-14
FRICH APPLICATION NUMBER: D2000-02-14
FRICH APPLICATION NUMBER: EPO 9870139.7
FRICH APPLICATION NUMBER: EPO 98870139.7
FRICH APPLICATION NUMBER: EPO 98870139.7
FRICH FILING DATE: 1998-06-18
FRICH APPLICATION NUMBER: EPO 97870122.5
FRICH APPLICATION NUMBER: EPO 97870122.5
FRICH FILING DATE: 1097-08-18
FRICH APPLICATION NUMBER: EPO 97870122.5
FRICH FILING DATE: 1097-08-18
FRICH APPLICATION NUMBER: EPO 97870122.5
FRICH FILING DATE: 1097-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%; Score 2174; DB 4; Length 711; 88.0%; Pred. No. 4.3e-154;
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| Sequence 22, Application US/07934373C |
| Patent No. 582137 |
| Patent INFORMATION: APPLICANT: Paul J. Carter |
| APPLICANT: Leonard G. Presta |
| TITLE OF INVENTION: Immunoglobulin Variants |
| NUMBER OF SEQUENCES: 48 |
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: SYNTHETIC US-09-485-7378-90
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Best Local S
Matches 409
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377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
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                                                                                         EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
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89.2%; Pred. No. 3.4e-153;
... w.ematches 28;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Generated, Inc.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                   437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
FILING APPLICATION DATA:
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 405; Conserva
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PCT-US93-07832-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk computer: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Geneticch) CURRENT APPLICATION DATA: O9-May-1995 CLASSIFICATION DATA: O9-May-1995 CLASSIFICATION DATA: APPLICATION MINDER: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION MINDER: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION MINDER: APPLICATION DATA: APPL
                                                       Sequence 22, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leconard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40,378
ER: P0709P2C1
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FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/922-9891
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
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Amino Acid
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US-08-437-642B-22
                        US-08-437-642B-22
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RESULT 12
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                                                                                                                     EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
                                                                                                                                                                                                                                     377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
                                                                                                                                                                                                                                                                                                 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EDELWAN, LENA
APPLICANT: MARCARITTE, CHRISTEL
APPLICANT: MACARITTE, CHRISTEL
APPLICANT: RAZZOREK, MICHEL
APPLICANT: CHABAIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS I
TITLE OF INVENTION:
NUMBER OF SUCURNES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: US/08/793,450 FILING DATE: 03-MAR-1997 PROFIGNATION: 536
                                                                                                                                                                                                                                                                                                                                        437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                        421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
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APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
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Patent No. 6312690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 703-413-2220
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MOLECULE TYPE: protein
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STREET: 17:
CITY: ARLIN
STATE: VA
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Sequence 14, Application US/08887352B
Sequence 14, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                      EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
                                                                                                                                                                       61 GOGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                  236 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
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                                                                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
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6
    Length 472;
                                         Indels
85.3%; Score 2147; DB 4;
85.1%; Pred. No. 2.6e-152;
live 26; Mismatches 37;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY ATTORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
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STATE: California
COUNTRY: USA
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1
  Query Match
Best Local Similarity 85.1<sup>§</sup>
Matches 404; Conservative
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                                          79 YNQKFKGKATLIVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
                                                                                                                                                                                                                                                                120 SSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179
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                                                                                                               Length 451;
                                                                                                                                             Indels
                                                                                                           84.5%; Score 2127; DB 2;
87.8%; Pred. No. 7.4e-151;
cive 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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ATORNEY/AGENT INFORMATION:
NAME: SVOBOda, Craig G,
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
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CITY: South San Francisco
STATE: California
COUNTRY: 0SA
             LENGTH: 451 amino acids TYPE: Amino Acid
                                                                                                                                             Conservative
SEQUENCE CHARACTERISTICS
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ADDRESSEE: Genenteck
STREET: 1 DNA Way
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Best Local Similarity
Matches 397; Conserv
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                                                             US-08-887-352B-14
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                                              TOPOLOGY:
                             TYPE:
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SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                        79 YNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                Length 451;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                           Query Match 84.5%; Score 2127; DB 2; Best Local Similarity 87.8%; Pred. No. 7.4e-151; Matches 397; Conservative 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER FEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
CORRESPONDENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WinPatin (Genentech)
                    TELEFAX: 650/952-9881
| INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 451 amino acids: TYPE: Amino Acid TOPOLOGY: Linear 105-08-887-352B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
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CITY: South San Francisco
STATE: California
: 650/225-1489
650/952-9881
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SOFTWARE: WinPatin
CURRENT APPLICATION DAY
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Gaps

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Indels

Length 451;

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240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14
                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                             84.5%; Score 2127; DB 4;
87.8%; Pred. No. 7.4e-151;
live 23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; LENGTH: 451
                 US/09/109,207C
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                                                                                                                                                                                                                                                             Best Local Similarity 87.8
Matches 397; Conservative
                                                                                                                   TYPE: PRT ORGANISM: Artificial
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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87.8%; Pred. No. 7.4e-151;
11ve 23; Mismatches 30;
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                                                                                               FILLING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09109207C Patent No. 617223
GENERAL INFORMATION: LOWING HEALT HENRY B. LOWMAN, LEONARD TITLE OF INVENTION: Improved Anti-I
                                            FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                               NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9811
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               397; Conservative
              APPLICATION NUMBER:
FILING DATE: 06-Jur
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Best Local Similarity
Matches 397; Conserva
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US-09-109-207C-14
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:19:01; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

US-09-499-662-147 2517 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_71:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qamma-1 chain	g gamma-3 chain	q qamma-3	g gamma-2a	ь	q qamma-4 chain		מ	g gamma-2b	- 67	-		g	Ig gamma 2a chain				gamma 1 chain	gamma chain C		gamma-2 chain		gamma-3 heavy	qamma-1 chain		qamma-1 chain			chain
SUMMARIES	QI		A23511	A60764	S37483	G2HU	G4HU	G2MS11	S40295	S01321	S22080	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	GIMS	PS0018	G1MSM	G3MSM
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	Query Match Length	330	377	377	469	326	327	474	446	475	470	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
æ	Query	8.69	65.1	65.1	64.0	64.0	63.5	61.4	61.3	29.7	58.7	58.4	57.0	56.8	50.3	50.1	49.8	49.5	49.1	48.9	48.9	48.1	46.3	•	•	•	45.5	•	45.3	45.3
	Score	1758	1639.5	1637.5	1610.5	1610	1599.5	1546	1544	1501.5	1477	1470	1435	1429.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
	Result No.	1	2	e	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56		28	29

Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
G2MSA	S00847	G2MSAB	G2MSAM	PS0019	S06611	GZMSBM	147162	S38864	S14683	S04845	S69131	S38950	A4944	869340	B46529
-	7	н	Н	7	7	~	7	7	7	7	7	7	7	~	7
330	329	335	399	322	327	405	277	548	627	549	241	246	220	249	572
44.9	44.8	44.8	44.7	44.3	43.4	42.9	42.5	39.7	37.6	36.8	34.6	33.8	31.8	30.4	30.3
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	666	946	925.5	870.5	851	801	765.5	762.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
	Tamma-1 chain C region - himan
	ty gammar I creator regions (man) (2. Species: Homo sapiens (man)
	C; Date: 31-Jan-1981 Firm
	C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
	R.Ellison, J.W.; Berson, B.J.; Hood, L.E.
	A:Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
	A93433; MUID:82274238
_	A; Accession: A93433
_	A, Molecule type: DNA A, a board digger in the control of the cont
_	A.Cross-references: EMBL: 217370
	A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
	A:Note: Lys-330 is removed after translation
	Rybarris, L.J.
	Subflicted to the Embi Data Library, October 1992 Sibelisted to the Embi Data Library, October 1992
	A, MCTETELICE IIIIIIIIIIEI: 533304 A: MCCESSion: 836861
	A: Molecule type: DNA
	A; Residues: 2-330 <har></har>
	R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
	Cell 29, 671-679, 1982
	A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of
_	A) Reference number: S33887; MUID:83001943
	A.A.Cession: Si388/
	A: Molecule type: DNA
	A,Kederrafoxonos BWB: 917370
	Arcuss Teleterances: Embirary 27 v Broundingham R A Burishanser II : Gall W E : Gottlieb D D : Waxdal M J : Edelma
	Biochemistry 9, 3161-3170, 1970
_	A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
	A; Contents: myeloma protein Eu
	A; Accession: B90563
	A; Molecule type: protein
	A.Note: this sequence has the Gim(3) marker, 97-Arg
	R. Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
	Biochemistry 9, 3171-3181, 1970
	A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
	A; Reference number: A90564; MUID:/IU64025
	A;Contents: Ed A:Anonesion: MOREA
	A.Modecule type: Drotein
	A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
	A, Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
	K)FOISLING!! H.; HISCHMAIN, N. Hobbe-Sevier's Z. Physiol. Chem. 357, 1571-1604. 1976
	Airitle: Die Primaerstruktur eines monoklonalen igg1-Immunglobulins (Myelomprotein Ni

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C. Accession: A23511
R: Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene A; Reference number: A23511; MUID:86148507
A; Accession: A23511
A; Molecule type: DNA
A; Residues: 1-377 < HUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; Cross-references: GDB:119339; OMIM:147120
A; Cross-references: GB:119339; OMIM:147120
A; Cross-references: GB:119339; OMIM:147120
A; Cross-references: GDB:119339; OMIM:147120
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                                          Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Homo sapieńs (man)
C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Accession: A60764
R.Huck, S.: Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an 1
A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 333
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local Similarity 82.8
Matches 312; Conservative
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Pred. No. 3.3e-93;
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      MUID:77070269
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99.1%;
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A; Reference number: A91668;
A; Contents: myeloma protein
A; Accession: B91668
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 537483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: 537483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-69 < DUC>
A;Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology < IMM>
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                                                           Length 377;
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llarity 64.4%; Pred. No. 1.2e-84;
Conservative 60; Mismatches 103;
                                                           5;
                                                        Score 1637.5; DB
Pred. No. 2.8e-86;
7; Mismatches 11
                                                                                                                                                                     201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV---
                 <IMM>
C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology
                                                         65.1%;
82.8%;
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Matches 312; Conservative
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Best Local Si
Matches 304
                                                         Query Match
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A; Molecule type: protein
A; Residues: 1-24, F., 256-57, FeV, 60-85;132-171, ZZZ',175, 'B',177-193, 'D',195-196,'Q',11,
A; Residues: 1-24, F., 256-57, EV, 60-85;132-171, ZZZ',175, 'B',177-193, 'D',195-196,'Q',11,
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A; Reference number: A93132; MUID:80114419
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A. Residues: 1-326 < ELL>
A. Kotes Sareferences: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A. Kote: Lys-326 is probably removed posttranslationally
B. Wang, A.C.; Tung, E.; Fudenberg, H.H.
T. Immunol. 125, 1048-1054, 1980
A. Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, a A. Contents: myeloma protein Til
A. Accession: A92809
A. Wolecule type: protein
A. Molecule type: prote
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C; Species: Homo sapiens (man)
C; Species: 30-Apr.1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Accession: A93906; A92809; A90752; A93132; A02148
R; Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy of A; Reference number: A93906; MUID:82197621
A; Accession: A93906
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A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90553; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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that shown in having
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A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
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A,Molecule type: DNA
A;Residues: 138-161, TL', 163-189, FP', 193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germl:
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blatti
Science 206, 1299-1303, 1979
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OMIM: 147130
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Best Local Similarity 91.8%;
Matches 303; Conservative
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                                                                                                                                                A;Genes: GDB:1GHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Genes: GDB:119338; OMIM:14828; OF The subunits associate into la G;Superfamily: immunoglobulin C region; immunoglobulin homology cIMI>
F;20-65/Domain: immunoglobulin homology cIMI>
F;20-50/Domain: immunoglobulin homology cIMI>
F;20-30/Domain: im
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440
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A; Reference number: A90933; MUID:83157104
A; Recession: A9093
A; Molecule type: DA
A; Residues: 1-327 < CLL>
A; Note: the sequence was determined from the germline gene
R; Pink, J:R.L.; Buttery, S:H.; De Vries, G.M.; Milstein, C.
B; Pink, J:R.L.; Buttery, S:H.; De Vries, G.M.; Milstein, C.
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of A; Reference number: A90249; MUID:70207560
A; Molecule type: protein
A; Residues: 1-30; 81-326 < PIN>
C; Genetics:
A; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                  G.
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                               A;Title: Structural studies of immunoglobulin A;Reference number: A93157; MUID:69064124 A;Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303; Conservative
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Matches
                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
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Ugamma-2b chain - mouse

C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 31-Mar-1980 #sequence_revision 01-Dec-2000
C; Accession: S25057; A02157; A26235; A26233; A35598
R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A; Description: Production of a Tobacco mosaic virus (TWV) inactivating neotop specifi A; Reference number: S25057
A; Accession: S25057
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1474 < FIS>
A; Cross-references: EMBL: K67210; NID:954826; PIDN:CAA47649.1; PID:954827
R; Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A; Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro A; Reference number: A02157; MUD:80120716
A; Roottents: a allele
A; Contents: a allele
A; Accession: A02157; August Augu
A position: 14932.33-14932.33

A introns: 99/1; 1117; 2217

A introns: 99/1; 1117; 2217

A introns: 99/1; 1117; 2217

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 
C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keyvords: duplication; glycoprotein; heterotetramer; immunoglobulin homology < IML>
F; 99-110/Region: hinge
F; 134-203/Domain: immunoglobulin homology < IML>
F; 144-207/Domain: immunoglobulin homology < IMS>
F; 144-307/Domain: immunoglobulin homology < IMS>
F; 147-1201,247-305/Disulfide bonds: interchain (to light chain) #status experimental
F; 177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1599.5; DB 1;
Pred. No. 3.4e-84;
9; Mismatches 15;
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C) Accession: S40295
R) Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C., aubmirted to the EMBL. Data Library, January 1993
A) Description: Primary structure of the murine monoclonal IgG2a antibody mab735 ag.in A) Reference number: S40295
A) Accession: S40295
A) Molecule type: protein
A) Residues: 1-446 < KLE>
C) Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin C region; immunoglobulin pyroglutamic acid
C; Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
E; 1-46/Product: Ig gamma-2a chain #status experimental <MAT>
F; 118-446/Promain: V-D-J region <VDJ>
F; 118-446/Pomain: C region <CHI>
F; 215-230/Region: hinge
F; 215-230/Region: hinge
F; 215-240/Pomain: C2 region <CHI>
F; 215-240/Pomain: C3 region <CHI>
F; 215-250/L440/Pomain: immunoglobulin homology <IMM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; 22-96, 144-199, 2561-321, 367-425/Disulfide bonds: interchain (to light chain) #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain #status predicted
F; 224, 227, 229/Pisulfide bonds: interchain #status predicted
F; 224, 227, 229/Pisulfide site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 07-Apr:1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                        PIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENN 413
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                                                                                                                                                                                                                 414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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Pred. No. 7e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-2a chain (mAb735) - mouse
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Best Local Similarity
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A,Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hear Ascassion: A5233; MUDD:80081501
A,Connents: MC 13
A,Connents: MC 14
A, Mass Tobaby removed posttranslationally 47
A,Title: Savines 183 1127 P, 174-189, FP',193-376, 'T',378-474 <TUD.
A,Hille: Savines 183 1127 P, MC 122
A,Hille: Savines and Savines A 2523; MUD:80081502
A,Hille: Savines immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Moterates b allot and munoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller bypes immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller bypes immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller bypes immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller bypes immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller byles immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller byles immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm A; Constiller and A; Constiller A; Massida K; Matsunaga C; Yamamoto, K; Irimura, T; Takahasi; A; Mccession: A56233
A,Cocassion: A56234
A; Mccession: A55294
A; Millianary
A; Mccession: A53599
A; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.4%; Score 1546; DB 1; Length 4 61.2%; Pred. No. 5.8e-81; indels ive 67; Mismatches 108; Indels
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Best Local Similarity 61.2
Matches 292; Conservative
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Gaps

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R.Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A; Reference number: $22080
A; Reference number: $22080
A; Reference number: $22080
A; Status: preliminary
A; Wolecule type: mRNA
A; Residues: 1-470 <SAN>
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
A; Residues: 0. 84.1-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A; Reference number: $06610; MUID:90097956
A; Residues: 142-470 <SXN>
A; Residues: 142-470 <SXN>
A; Residues: 142-470 <SXN>
A; Residues: 142-170
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Genetic
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Sacession: S31459
R;Patri, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
S;Beference number: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ALEWVGGI-TSGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.7%; Score 1477; DB 2; 60.4%; Pred. No. 4.8e-77; ive 62; Mismatches 115;
   C; Accession: S22080; S06610; A31303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.7%
Best Local Similarity 60.4%
Matches 285; Conservative
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                                                                                                                                                                                                                                                                                    Use gramma-2b chain precursor - mouse

C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: 501321
R;de Waele, P:; Feys, V; van de Voorde, A.; Molemans, F.; Fiers, W.
R;de Waele, P:; Feys, V; van de Voorde, A.; Molemans, F.; Fiers, W.
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: 50132;
A;Reference number: 50132;
A;Reference number: 50132;
A;Molecule type: mRNA
A;Residues: 1-475 cbell>
A;Residues: 1-475 cbell>
A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A;Cross-references: EMBL:X13188; NID:951780; Minunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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N;Alfernate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;pate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 WNSGSLSSSVHTFPALLQ-SGLYTMSSSYTVPSSTWPSQTVTCSVAHPASSTTVDKKLEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 1501.5; DB 2; Length
60.6%; Pred. No. 2e-78;
ive 66; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:1-19/Domain: signal sequence #status predicted <SIG>F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>F:159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                       415 KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                         438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Best Local Similarity
Matches 289; Conserv
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C. Species: Homo sapiens (man)
C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C. Accession: S69339; S72664
R. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A. Fitle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A. Reference number: S69339
A. Reference number: S69339
A. Status: praliminary
A. Molecule type: mRNA
A. Residues: 1-374 < KHA>
A. Cross-references: EMBL:X81695
R. Khamilchi, A.A.
Submitted to the EMBL Data Library, September 1994
A. Reference number: S72664
A. Recession: S72664
A. Residues: 1-140, 'C', 142-374 < KH2>
A. Cross-references: EMBL:X81695
C. Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                GLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
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                                                                                                                                                                                                                                                              3 WT--LLFVLSAPRGVLSQVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGK 60
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                                                                                homology
                                                                                                                                                              tch 58.4%; Score 1470; DB 2; Length 4 al Similarity 59.6%; Pred. No. 1.2e-76; 283; Conservative 66; Mismatches 114; Indels
          A;Status: preliminary
A;Mceule type: mRNA
A;Mceule type: mRNA
A;Residues: 1-472 - CPAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
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Best Local S:
Matches 283
A; Accession:
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Graduoclonal antibody 13-1 heavy chain - mouse (fragment)
Gradies: Mus musculus (house mouse)
Gradies: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
Gracession: PC4436
Gracession: PC4436
Grado, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
Aritle: Structural characterization of mouse monoclonal antibody 13-1 against a porfaraccession: PC4436
Arcession: PC444 < ARA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                        SNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
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Length 374;
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Score 1435; DB 2;
Pred. No. 9.2e-75;
/; Mismatches 58;
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    57.0%;
60.1%;
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Search completed: August 14, 2002, 15:19:02 Job time: 690 sec
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Best Local Similarity 69.6%;
Matches 231; Conservative 41
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C; Species: Sus scrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147159
R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Titler: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID:95012845
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C;Genetics:
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69.9%; Pred. No. 2.9e-65;
ive 42; Mismatches 52;
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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Rikacskovics, I: Sun, J: Butler, J.E.
A:Title: Five putative subclasses of swine IgG identified from the CDNA seq A; Feference number: 147158; MUID:95015845
A; Accession: 147160
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A; Accession: 147160
A; Mulcule type: mRNA
A; Residues: 1-328 < KAC>
A; Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C; Genetics:
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F;133-202/Domain: immunoglobulin homology <IMM>
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; Pred. No. 6.4e-65;
41; Mismatches 54;
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Database :

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SUMMARIES	ID	GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC_RABIT	GC2_CAVPO	GC3_HUMAN	GC1_RAT	GC3_MOUSE	GC1_MOUSE	GCB_RAT	GC1M_MOUSE	GC3M_MOUSE	GCAA_MOUSE	GCC_RAT	GCAB_MOUSE	GCAM_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	HV07_MOUSE	HV06_MOUSE	HV11_MOUSE	HV48_MOUSE	HV05_MOUSE	HV02_MOUSE	HV09_MOUSE	HV04_MOUSE	EPC_RAT	EPC_HUMAN	HV49_MOUSE		HV10_MOUSE	HV15_MOUSE
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## ALIGNMENTS

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HHUMAN  557.  10.  11.  12.  13.  14.  15.  16.  17.  17.  17.  17.  17.  17.  17	STANDARD;	(Rel. 01, Creat (Rel. 01, Last (Rel. 40, Last hain C region.	(Human). etazoa; Chordata; theria; Primates; 606;	M N.A. 4238; PubMed=6287, Berson B.J., Ho ide sequence of a s Res. 10:4071-4(	1-135 (MYELOMA PF 4024; PubMed-5489 .A., Rutishauser Edelman G.M.; t structure of a	9:3161-3170(1970 136-329 (EU). 4025; PubMed=5530 U., Cunningham B.	; t structure of a e of heavy-chain 9:3171-3181(1970	ELOWA PROTEIN NIE 0269; PubMed=8264 Hilschmann N.; antibody structur gGl immunoglobuli peptides of the discussion of th 's Z. Physiol. CP	ELOMA PROTEIN KOI 9131; PubMed=6884 , Jung HD., Pal sional structure crystallized mon 's Z. Physiol. CP	NDS. 4027; PubMed=4923
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                                                                                                                                                     "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
Blochemistry 20:231-2370(1981).

Hiscellanbous: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-I- MISCELLANBOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-I- MISCELLANBOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155,166,177,195,198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                                 Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal light immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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R InterPro; IPR003507; Ig_cl.
R InterPro; IPR003507; Ig_cl.
R InterPro; IPR003507; Ig_lake.
R Fam; PF00047; Ig_lake:
R SWART; SW00410; IG_like: 1.
R SWART; SW00407; IG_like: 1.
R SWART; SW00290; IG_MHC; 2.
R Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D_structure.
I DOMAIN 99 110 HINGE.
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D -> E (IN GIM(NON-1) MARKER).
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PIR; A02146; GHU.
PDB; IFC1; IS-JUL-92.
PDB; IFC2; IS-JUL-92.
MIM; 147100; -.
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                                          MEDLINE-77070267; PubMed=1002129;
        Biochemistry 9:3188-3196(1970).
 Intrachain disulfide bonds.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
IGHGamma-2 chain C region.
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MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
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MEDLINE-80001357; PubMed-113060;
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"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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                                              Ellison J.W., Hood L.E.; "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes."; Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
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"The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of
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Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                             SEQUENCE OF 99-177 AND 310-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
MEDLINE=81007873; PubMed=6774012;
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MEDLINE=95255298; PubMed=7737190;
                        SEQUENCE OF 2-326 FROM N.A. MEDLINE-82197621; Pubmed-6804948;
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Mol. Immunol. 16:923-925(1979).
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Cell 29:671-679(1982).
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SEQUENCE OF 238-275 (ZIE)
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 NCBI_TaxID=9606;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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Pred. No. 8.9e-104;
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NON TER 1 98 רדו 98
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91.8%; Pred. No. 8.9e.
+ive 10; Mismatches
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003590; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
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                                                                                     EMBL; J00230; AAB59393.1; -. PIR; A02148; G2HU.
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MIM; 147110; -
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
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                                                                                                                                              SEQUENCE OF 1-30 AND 81-326.
MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                    Ellison J.W., Buxbaum J.N., Hood L.E.; "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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INTERCHAIN (WITH A HEAVY CHAIN)
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 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                 SEQUENCE FROM N.A.
MEDLINE-83157104; PubMed-6299662;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_Like; 1.
PROSITE; PS00290; IG_MHC; 2.
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91.8%;
          gamma-4 chain C region
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                              Homo sapiens (Human)
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HSSP; P01842; 7FAB.
MIM; 147130; -.
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327 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
HISCELANDENGS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.
                              MIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
imminarials." "
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MEDLINE-83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    323 AA
                                                                                                                                            QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                               298 QEGNVFSCSVMHEALHNHYTQKSLSLGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84030930; PubMed-6313520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-128.
MEDLINE-76135469; Pubmed-1243651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-70110015; PubMed-5461106;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC
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                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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SEQUENCE FROM N.A.
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Biochemistry 10:26-31(1971).
-!- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 IMPRED GUINEA PIGS.
PIR; A02151; G2GP.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=71058474; PubMed-4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
Birshtein B.K., Hussain Q.Z., Cebra J.J.; Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
                                                                                                                     carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 134-226.
MEDILINE-7036072; Pubmed-4429665;
Tracey D.E., Cebra J.J.;
"Primary Structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                          MEDLINE-75036073; Pubmed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig 19G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTH--TCPPCPAPEL
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
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                                                                                                           pig
the
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                                                                     SECUENCE OF 69-133 AND 312-329.

MEDLINE-71058466; PubMed=5538616;

Turner K.J., Cebra J.J.;

Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                           Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                          Biochemistry 13:4804-4811(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P01772; ZFB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig_ 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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308
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329 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 443
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                         Cávia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                               DB 1; Length 323;
                                                                                                                                                                                                                                                                                              Query Match 48.9%; Score 1231.5; DB 1; Length Best Local Similarity 70.0%; Pred. No. 9.1e-78; Matches 229; Conservative 34; Mismatches 57; Indels
                                                                    M (IN D11 MARKER).

A (IN B15 MARKER).

E (IN REF. 2).

VPV (IN REF. 2).

E (IN REF. 5).

D (IN REF. 5).

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      Immunoglobulin domain;
      Immunoglobulin C region.

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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
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                                                                         SEQUENCE OF 4-68.
MEDLINE=71058471; PubMed=5538606;
                                                                       HHZ>OZOZOMZMZ
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                         400407; IGC1; 2.
PS00290; IG_MHC; 1.
  InterPro; IPR003597; Ig_cl
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1173
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               SMART; SM00407; 1GC
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P01862;
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                            235
                                                         378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 435
                                                                        MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM
318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISCUFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISCUFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.

-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                                       Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prihany structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                MEDLINE-82247835; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE-77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin B.C.;
"Primary structure of the 'hinge' region of human igg3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-301 (Rel. 40, Last annotation update)
169 gamma-3 chain C region (Heavy chain disease protein) (HDC)
1GHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Franglone B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein 20C. Structure of the Fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
                                                                                                                436 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
                                                                                                                               296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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MEDLINE-81021548; PubMed-6774747;
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                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
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F -> Y (IN OMM).
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S -> N (IN OMM).
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r -> A (IN OMM).
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                                                                                                                                   HSSP, P01857; IFC1.
MIM: 147120; ...
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                          IR; A02149; G3HUWI.
SSP; P01857; 1FC1.
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GC3_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1989).
PIR; PSO017; PSO017.
HSPP: P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
From PF00047; Ig. 3.
SMART; SM00407; Igc1; 2.
PROSITE; PSO0290; IG_MHC; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                     419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-gamma-1 chain C region.
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MEDLINE-89232738; PubMed-3149946;
Brueggemann M.;
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326 AA;
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P20759;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed=6092053;
MEDLINE=85027161; PubMed=6092053;
MELS J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine igg3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01857; IECI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
IMMINOSITE; PS00299; IGMUC: 1.
Imminoglobulin domain; Imminoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
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65.0%; Pred. No. 3.7e-72;
ive 44; Mismatches 68;
                                                                                                                                                                                                                                     update)
                                                                                                                                       329 AA
                                                                                                                                                                                                          Last sequence update)
Ig gamma-3 chain C region, secreted form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                        Last annotation
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Matches 215; Conserv
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01-AUG-1991 (
16-OCT-2001 (
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SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILINE-80012837, PubMed-113776;
ROGERS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).

MEDLINE-80202559; PubMed-6769752;

Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,

Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;

"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";

Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Cloning and complete nucleotide sequence of mouse immunoglobulin
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MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-80045036; Pubmed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami
Takahashi N., Mano Y.;
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                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
23-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                         324 AA.
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"Evolution of immunoglobulin subclasses.
murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                   299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PIR; A02199; GAA24176.1; -.
HSSP; P01842; 77F8.
                                                                                                                                                                                                                                                                                         STANDARD;
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Cell 18:559-568(1979).
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P01868;
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GC1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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GlycoSuiteDB; P01868; -.
MGD; MGI:56446; Igh-4.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR00300597; Ig_Cl.
Pfam; PF00047; ig; 3.
SWART; SMO407; IG, 12.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                            35704 MW;
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Matches 207; Conservative
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                                                                                                                                 Alternative splicing,
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276
278
324 AA;
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Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988). PRIX; PS0018; PS0018. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                            ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS-----CDKTHTCPPCPA 254
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus
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                                                                                                                                                      CHAIN).
CHAIN).
CHAIN).
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                                                                                                PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
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01-AUG-1991 (Rel. 19, Last seq
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80
106
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333 AA;
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P01869;
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoapilobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                                                         Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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MEDLINE-82115295; Pubmed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
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                                                                                                                                                                                                                                                                                                                                 "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.", cell 26:19-27(1981).
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4CC88343B7A1CE27 CRC64;
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                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
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55; Mismatches
[2]
SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; Pubmed-6804950;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-44 FROM N.A.
MEDLINE-82222190; PubMed=6283537;
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EMBL; V00793; CAA24173.1; -
EMBL; V00793; CAA24174.1; -
EMBL; V00793; CAA24174.1; -
EMBL; V00793; CAA24174.1; -
EMBL; W00793; CAA24174.1; -
HSSP; P01842; 7FAB.
MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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IGc1; 2.
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Best Local Similarity
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SMART; SM00407; IGC
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393 AA;
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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                                                                                                                    201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                             Wall R.; "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                 259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Musinse
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MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
HSSP; P01687; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003609; Ig_Like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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P03987;
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SECUENCE FROM N.A.
MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 398;
                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

E -> G (IN REF. 2).

E -> C (IN REF. 2).

P -> F (IN REF. 2).

W; CF7F264B50A41B95 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-MAY-2000 (Rel. 39, Last annotation update)
1g gamma-2A chain C region, A allele.
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HINGE.
   Alternative splicing
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SEQUENCE FROM N.A.
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Transmembrane; R
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DOMAIN 98
DOMAIN 114
DOMAIN 224
TRANSMEM 346
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P01863;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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"Determination of the primary structure of a mouse 1gG2a immunoglobulin.amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                               suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                           "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%; Score 1129; DB 1; Length 330; 63.9%; Pred. No. 1e-70; ive 43; Mismatches 73; Indels
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B84361C5445A6864 CRC64;
                                                                          Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain; Immunoglobulin C region.
                                                                                                     MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
MEDLINE=81223894; PubMed=6787604;
Ollo R., Auffray C., Morchamps C.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
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                                                              RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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HINGE.
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MEDLINE=88166903; Pubmed=3127222;
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
Interpro; IPR003500; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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329 AA;
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                                                                                                                         LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
                                                                                                                                                                                                                                                        378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2A chain c region, B allele.
Mus musculus (Wouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Dognin M.J., Lawwereys M., Strosberg A.D.;
"Multiple amino acid Substitutions between murine gamma 2a heavy chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78 44031-40351(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D Schreier P.H., Bothwell A.L.M., Mueller acid sequences of "Multiple differences between the nucleic acid sequences of IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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HSSP; P01857; 1FC1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG.11ke; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG.MHC: 1
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P01864;
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Score 1126.5; DB 1; Length 335; Pred. No. 1.6e-70;

44.88; 61.68;

Best Local Similarity

Query Match

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141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                        GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK-----SCDKTHTCPPCPA 254
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7; Gaps
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Mismatches
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52;
Matches 207; Conservative
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REALINE-27BL/G5. TISSUE-PANCREAS;

REALINE-21085660; PubMed=11217851;

RA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Chriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Fuuno M., Aono H., Baddarelli R., Barsh G.,

RA Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nayashirak B., Nayashirak K., Weitz C., Whittaker C., Wilming L.,

M. Wynshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Havashiraki Y.,

A Havashiraki Y.,

M. Wasashiraki Y.,

M. Wasashiraki Y.,

M. Wasashiraki Y.,

M. Wasashiraki Y., Storch K.-P.,

M. Wasashiraki Y., Saboraki Y., Kawaji H., Kohtsuki S.,

M. Wasashiraki Y., Kawashiraki S.,

M. Wasashiraki Y., Kawashiraki S.,
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Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EMBL; AKO07918; BAB25349.1; -.
HSSP; P01842; 7FAB.
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01-JUN-2001 (TrEMBLEE).
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1810060009RIK PROTEIN.
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Q96dk0
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB
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Interpro: IPR003599; Ig.
Interpro: IPR003599; Ig_cl.
Interpro: IPR003600; Ig_like.
Interpro: IPR003006; Ig_like.
Interpro: IPR003006; Ig_lv.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
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Submitted (FEB-2001) to the
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC
                                                                                                                                                                      Query Match 64.65
Best Local Similarity 63.65
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
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                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                    9DED57A514475FBB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                              65.0%; Score 1636.5; DB 1:
63.7%; Pred. No. 5.6e-129;
Live 70; Mismatches 94;
                                                                                                                                                                   PS00290; IG_MHC; UNKNOWN_1
473 AA; 51699 MW; 9DED
      InterPro; 198003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003507; Ig_cl.
InterPro; IPR003006; Ig_Hke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IG; 2.
SMART; SM00407; IG; 1.
SMART; SM00407; IG_ILike; 1.
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InterPro; IPR003597; 19_c1.
InterPro; IPR003600; 19_like.
                                                                                                                                                                                                                                                             303; Conservative
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4GD; MGI:96443; Igh-1.
                                                                                                                                                                                                                                                Similarity
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Best Local Si
Matches 303,
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61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSYTVPSSTWPSETVTCNVAHPASSTKVDKKIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 RDCG----CKPCICTVPEV---SSVFIFPPKPVLTITLTPKVTCVVVDISKDDPEVQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 ISKAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                      64.6%; Score 1625.5; DB 11; Length 463; 63.6%; Pred. No. 4.6e-128; ive 72; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 3.

SMART; SM00407; IG; 2.

SMART; SM00407; IGv; 1.

SMART; SM00406; IGv; 1.

SMART; SM004107; IG_Like; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                                                                                                                                                                                                                            VKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
                                                                                                                                                                                                                                                                                                                                                                415
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                                                                                                                                                       61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                             Gaps
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                                                                                                                           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                               121 --YSNN-WYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                        178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR
                                                                                                                                                                                                                                                                                                                                                               EKTISKAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYK
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 1585.5; DB 11; Length 473; 63.4%; Pred. No. 1.1e-124; Live 61; Mismatches 106; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Strausber No.

L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; BC003878; AAH03878.1; -.

R EMBL; BC003878; AAH03878.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003006; Ig.—Ike.

R InterPro; IPR003006; Ig.—MHC.

DR SMART; SM00407; Ig; 4.

DR SMART; SM00409; IG; 2.

DR SMART; SM00409; IGc.1; 3.

DR SMART; SM00400; IGc.1; 3.

DR SWART; SW00410; IGc.1; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                Best Local Similaricy Autohes 301; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                      Query Match
Best Local Similarity
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
antibody (Mab 7, its light and heavy chains) and construction of a
antibody (Mab 7, its light and heavy chains) and construction of a
submitted (MaY 1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF152372; AAD40243.1; -.

R HSSP; P01842; 7FAB.
R HSSP; P01842; 7FAB.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003506; Ig_MHC.
R FART; SM00406; IG_Like; 2.
R SMART; SM00410; IG_Like; 2.
R RART; SM00410; IG_Like; 2.
R RART; SM00410; IG_Like; 2.
R RART; SM00410; IG_Like; 2.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                    YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                          WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFILA;

O1-MAY-2000 (TrEWBLrel. 13, Created)

O1-MAY-2000 (TrEWBLrel. 13, Last sequence update)

O1-DEC-2001 (TrEWBLrel. 19, Last annotation update)

GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TAXID=10090;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 468;
                                                                                                                              Indels
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96352328B3332ADB CRC64;
                                                                       Query Match 61.9%; Score 1559; DB 11; Best Local Similarity 62.7%; Pred. No. 1.8e-122; Matches 296; Conservative 62; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
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51661 MW;
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SEQUENCE FROM N.A.
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468 AA;
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                                                                                                                                                                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 MGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 --FDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                  --SSVFIFPPRPKDKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                    21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNYN
                                                                                                                                                                                                                                                                    259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                             EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.6%; Score 1423.5; DB 11; Length 473; 57.1%; Pred. No. 4.2e-111; Live 74; Mismatches 114; Indels 15;
 DB 11; Length 437;
                            17;
                         96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001).
SEMBL, BC010327, AAH10327.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091205 PRELIMINARY; PRT; 473 AA.
091205;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
            Pred. No. 3e-112;
57.1%; Score 1436.5;
59.3%; Pred. No. 3e-1
                         71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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              Similarity
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 Query Match
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MEDINE-98383416; PubMed-9717671; Wagner B., Oreresch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Corganization of the equine immunoglobulin heavy chain constant region "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c.mu, c.gamma, c.epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
             ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
                                                                                                       FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP-----KSCDKTHTCPPCPA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                    KT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                           TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 337;
                                                                                                                                                                                                            418 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.2%; Score 1263.5; DB 6; ilarity 68.9%; Pred. No. 6.9e-98; Conservative 44; Mismatches 52;
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                                                                                                                                                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, IMMUNGGOBULIN GAMMA 1 HEAVY
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 233; Conserv
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SEQUENCE
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                      240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
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375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Targeting tissue factor on tumor vascular endothelial cells an cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AAK58686.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1257; DB 4; Length 701;
Pred. No. 6.9e-97;
2; Mismatches 0; Indels (
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18686.1; -. 77826 MW; 94AC6CEB42CC992F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                      LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-21477448; PubMed-11593034;
Hu Z., Garen A.;
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01-DEC-2001 (TrEMBLTel. 19, Last
UNKNOWN (PROTEIN FOR MGC:18977).
Mus musculus (Mouse).
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99.1%;
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Best Local Similarity 99.1
Matches 230; Conservative
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Mammalia; Eutheria;
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Q96PQ8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YSNNW--YFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
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                                                                                                1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                         180 WNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.0%; Score 930.5; DB 4; Length 614; 36.7%; Pred. No. 1.4e-69; ive 84; Mismatches 166; Indels 115;
                                         ..
8
Length 278;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. STEF536E77AA9BBB CRC64; GT921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
  Score 983; DB 11;
Pred. No. 1.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                     241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
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                                         Mismatches
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Eukaryota; Metazoa; Chordata;
  39.1%;
67.1%;
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Best Local Similarity 36.79
Matches 212; Conservative
                                         Conservative
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                       Matches 186;
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                                                                                                                                                                       PSREEMT-KNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
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----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                        MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|: | :: || :| || || || SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQH-DSNPVQELNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%; Score 887.5; DB 11; Length 481; 42.7%; Pred. No. 4.1e-66; Live 73; Mismatches 172; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-COLON;
Strausberg R.;
Submitted (SER.
Submitted (SER.
EMBL, BC011488; AAH13488.1; -..
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                     431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                                                                                                                                                                                                                                                                                                                                 481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL 52.0 KDA PROTEIN.
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Best Local Similarity 42.7%
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91WT3;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                               091WT3
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Q91WT3
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18;
DYS---NNWYF---DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPSQDVTV-----PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLTVLHQD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNHKPS
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 862; DB 4; Length 500; 41.3%; Pred. No. 6e-64; Live 67; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005951; AAH05951.1; -. HSSP; P01789; IMCP. InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HOMPO SADJENS (Human).
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0; IG_MHC; UNKNOWN_1.
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InterPro; IPR003600; 19_11ke.
InterPro; IPR003066; 19_MHC.
InterPro; IPR003596; 19_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 1g; 4.
SMART; SM00409; 1G; 4.
SMART; SM00407; 1Gc1; 2.
SMART; SM00410; 1Gc1; 2.
SMART; SM00410; 1G_11ke; 1
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                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00290; IG
Hypothetical protein.
SEQUENCE 500 AA; 5
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hes 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                    470
                                                                                         463
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Matches
                                                    469
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Query Match
Best Local Simi
Matches 191;
                          Q91WR1;
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Q96BB9
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              121 YSNNWYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGGWAEDYWGQGTTLTVSSEPAREPTIYPLT-FFQALSSDPVIIGCLIHDYFPSGTMNV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 NCPGICSPPTTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                       091WI1;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mus musculus (Mouse)

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENNYKTTPPVLDSDG - - SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                       Length 481;
                                                                                                                                                                                                                                                                                                                                                                    33.1%; Score 833.5; DB 11; Length 40.2%; Pred. No. 1.4e-61; Live 73; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013490; AAH13490.1; - Hypothetical protein. SEQUENCE 481 AA; 52105 MW; 97DFGBDI59463F65 CRC64;
                                                                                                                                 481
                                                                                                                                 PRT;
                                                         | |||| :||::: || VGHEALPLAFTQETIDRLAGK 482
                                             VMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.1%
Best Local Similarity 40.2%
Matches 194; Conservative
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           TISSUE=COLON;
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                                                                                                                              Q91WT1
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121 YSNNWYF-----DVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 PEGAVFTW-----PSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 ALPAPIEKTISKAKGOPREPOVYTLPPSREEMTKNO-VSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; 8C013539; AAH1339.1; -. Hypothetical protein. SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                          11 protein.
488 AA; 52964 MW; F12068460B400B9D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
                                                                    Last sequence update)
Last annotation update)
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                                         01-DEC-2001 (TrEMBLrel. 19, Cr. 01-DEC-2001 (TrEMBLrel. 19, La. 01-DEC-2001 (TrEMBLrel. 19, La. HYPOTHETICAL 53.0 KDA PROTEIN. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=10090;
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464 IDRLSGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYT 373
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                                                                                                                                                                                                                                                           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                             231 N-----TKVDKRVEPKS------CDKTHTCP-----
                                                                                                                                                                                            Ouery Match 32.4%; Score 815.5; DB 4; Length 597; Best Local Similarity 32.6%; Pred. No. 6.2e-60; Matches 190; Conservative 94; Mismatches 179; Indels 119;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
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Mammalia; Euther
NCBI_TaxID=9606;
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Search completed: August 14, 2002, 15:22:19 Job time: 687 sec

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August 14, 2002, 15:15:40 ; Search time 230.21 Seconds (without alignments) 226.770 Million cell updates/sec
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1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTGKSLSLSPGK 470
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:* A_Geneseq_032802:* 1: /stnc1 /~--Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Humanised anti-Fas	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Humanised HMFG-1 h
SUMMARIES	AAW90936	AAW83037	AAB14779	AAW90929	AAW90935	AAW90934	AAW90933	AAW83036	AAB14776	AAW90926	AAM52156
DB	77	19	21	21	21	21	21	19	21	21	22
Length	470	470	470	470	470	470	470	470	470	470	731
% Query Match Length DB	100.0		99.5								
Score	2518	2498	2498	2498	2498	2497	2495	2485	2485	2485	2363.5
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(SANY ) SANKYO CO LTD.

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Humanised HMFG-1 h	Humanised HMFG-1 h	HMFG-1	Humanised HMFG-1 h	7.5	<b>A</b> 3	Heavy chain of hmA	Humanised 323/A3 (		Monoclonal antibod	Chimeric 2403 IgG	Sequence of antibo	Human reshaped F19	Antibody D heavy c	Completely humanis	ĽΩ	Ganglioside GM2 an	Recombinant immuno	Humanised anti-IL-	Humanised anti-IL-	Human immune syste	Anti-IL-8 humanise	Human novel protei	Human type antihum	Chimeric mouse/hum	Human type antihum	Human type antihum	Amino acid sequenc		D9D10 heavy chain	MoTAbII fusion pro		Anti-5T4 single ch	Reshaped CAMPATH-1
AAM52159	AAM52158	AAM52161	AAM52157	AAM52160	AAB72228	AAW48650	AAB72232	AAB08026	AAW88464	AAE03755	AAR24442	AAY50166	AAR31023	AAR43339	AAW49816	AAB83156	AAY29458	AAB30322	AAY77766	AAB36210	AAW69316	AAU14177	AAG64475	AAY50157	AAG64471	AAG64469	AAG63640	AAG64473	AAW85689	AAW85692	AAB83838	0	AAR22757
22	22	22	22	22	22	19	22	21	20	22	13	20	14	14	19	22	50	21	21	22	19	22	22	20	22	22	22	22	20	20	22	20	13
741	729	739	730	740	465	652	464	470	476	466	481	472	476	449	449	583	452	452	452	467	452	474	473	472	473	473	475	473	468	711	265	595	470
93.9	93.7	93.7	93.4	m	Ξ.	0	0	0	٥.	6	σ.	8	8	æ	ω,	8	7	۲.	۲.	7.	۲.	7	7	7.	7.	9	٠,	9	9	٠,	٠,	86.1	5.
363.	2358.5	35	35	35	29	2289	2286.5	2274	2269	2264	2259.5	2238	2238	2230	2230	2219.5	2210.5	2210.5	2210.5	2207.5	2201.5	2193	2192.5	2190	2189.5	84.	183.		^	7	~	2168	9
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-alleristic, anti-architic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, antinfactility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthitis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, soleroderma, sterility, myasthenia gravis, antither sclerosis, Basedow's disease, thrombopenia purpura, insulin and part and antity 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fullniane, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mind the native ligand, do not induce liver disease, and have reduced risk of a human anti-nurine antibody response. This sequence represents a humanised anti-Fas antibody HEFTA heavy chain construct HHH type
                                                                                                                                                                                                                     New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                        Tamaki I, Takahashi T;
                                        Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 188-189; 263pp; English.
                                        Haruyama H,
                                                                                                            WPI; 2000-258930/23.
                                                                                                                                                    N-PSDB; AAA11655
                                        Serizawa N,
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; 0 420 61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 Gaps 1 mgwsciilflvatatgvhsgvqlvqsgaevkkpgasvkvsckasgytftsywmgwvrqap 60 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 1 MGWSCIILFLVATATGVHSOVOLVOSGAEVKKPGASVKVSCKASGYTFTSYWMOWVROAP ; 0 Length 470; 0; Indels Score 2518; DB 21; Pred. No. 1.4e-144; 100.0%; Scor. 100.0%; Pred. No. 1... 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 470; Conservative 61 181 301 361 301 g à 엄 à g ò 엄 ò a ò g à

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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                KW apoptosis; HFE7A; autoimente disease; Has; humanised antibody; apotosis; HFE7A; autoimente disease; Hashimoto's disease; KW systemic lupus erythematosus; graft versus host disease; KW scleroderma; Goodpasture syndrome; Crohn's disease; Sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; W rheumatoid arthritis; autoimmune haemolytic anaemia; thrombopenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; W qtopy; arteriosclerosis; myocarditis; cardiomyopathy; W glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                           Jun O, Kimihisa I;
, Tohru T;
                                                                                                                                                                                                                                                                                                                                                Anti-Fas humanised antibody HFE7A heavy chain.
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/label- Mat_protein
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O, Nobufusa S, Shin Y,
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/label= variable
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/label= CDR_H1
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                                                                                                                                                                                                                                       AAW83037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 yvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are conserved in the human IgG heavy chain. Host Escherichia colipgipubly 3 Sark 7028 harbors plasmid pgHPDHY3 carrying a fusion fragment of the humanised HV type HFB7A heavy chain and DNA encoding human IgGl constant region (see AAV70080), and is deposited as FERM BP-6273 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFB7A (see AAW83031-37), like native HFB7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to
                                                                                                                                                                                                                                                                                                                                           treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple scl rosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allerqise, atopy, arteriosclerosis, anyocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                  This is the amino acid sequence of the HV type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. It includes humanising R44G and A76T amino acid substitutions that are are conserved in the human IgG heavy chain. Host Escherichia coli
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Pred. No. 2.3e-143;
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                  Claim 22; Page 225-227; 292pp; English.
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Best Local Similarity
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                                                               Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caused by an abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
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                                Humanised anti-Fas antibody heavy chain, SEQ ID NO:117
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Pred. No. 2.3e-143;
3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page 108-109; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFE7A-derived anti-Fas antibodies.
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98.9%;
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                                                                                                                                                                                       - Mus musculus.
- Homo sapiens.
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Best Local Similarity
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Chimeric
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AAB14779 standard; Protein; 470 AA

AAB14779

AAB14779;

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; systemic lupus erythematosus; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sollerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule (1) that, induces apoptosis in cells with a abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases associated with the Fas/Fas ligand system, especially systemic
                                   241 kscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
                                                                                                              361 KAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                             Takahashi
                                                                                                                                                                                        421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised HFE7A designed heavy chain protein #2.
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                                                                                                                                                                                                                                                                                                                        AAW90929 standard; Protein; 470 AA.
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                versus host disease, Sjorgen's syndrome, pernicious or hypopiastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEFTA designed heavy chain which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunownodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
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graft
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                                                                                                                                                                                                                                                                                                                                                               Score 2498; DB 21;
Pred. No. 2.3e-143;
3; Mismatches 2;
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98.9%;
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Best Local Similarity 98.9
Matches 465; Conservative
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This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
capptosis in cells with a normal system, by inhibiting binding between
capptosis in cells with a normal system, by inhibiting binding between
canti-anemic, antidiabetic, anti-alergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
cantilatoric cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to cell surface Fas or inhibit it by competitive
capptosis by binding to salfamers system, especially systemic
lupus erythematosus, Hashimoto disease, remaina, apoptosis
clupus erythematosus, Hashimoto disease, remaina, apoptosis,
canemia, Addison's disease, scleroderma, sterility, myasthenia gravis,
and the sclerosis, Basedow's disease, thrombopenia purpura, insulin
callatory, alomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(C) inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
mutine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-Pas antibody heavy chain construct designated Heu 3
which is described in the method of the invention.
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Goodpasture syndrome, Crohn's disease, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, allergy, insulin dependent diabetes mellitus; arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis, transplant rejection.
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Pred. No. 2.3e-143;
3; Mismatches 2;
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98.9%;
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                                                                                                                  Synthetic.
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anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotrophc; antinfertility; neuroprotective; antiarteriosclarotic; hepatotropic; humanized; apoptosis; systematic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
300
                                                                                                                                                                      360
                                                                                                        241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                 361 kakgqprepqvytlppsreemtknqvs1tc1vkgfypsdiavewesngqpennykttppv 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                            WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                      301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                    KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                   Takahashi T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised anti-Fas designed heavy chain Heu 2 protein.
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98JP-0276882.
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30-SEP-1998;
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Humanised anti-Fas designed heavy chain Heu 1 protein.

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dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardlomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (b. Cor D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.
apoptosis in cells with a normal system, by inhibiting binding between fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyronimetic, antianteriors, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, soleroderma, goodpasture syndrome, crohn's disease, altolumune hemolytic anemia, sterility, myasthenia gravis, and the solerosis, Basedow's disease, thrombopenia purpure, issulin
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470 AA; Sequence

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                                                                                                                                                                301 yvdgvevhnaktkpreegynstyrvvsvltvlhgdwlngkeykckvsnkalpapiektis 360
                           Gaps
                                                               1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
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                                                                                                                                                                                                                                                                                                                                                      KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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99.2%; Score 2497; DB 21; Length 470; 98.9%; Pred. No. 2.6e-143;
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                        Indels
                        3; Mismatches
                        465; Conservative
             Similarity
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Matches 46
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AAW90933 standard; Protein; 470
                                             08-AUG-2000 (first entry)
                            AAW90933;
AAW90933
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Gaps

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Indels

Ouery Match 99.1%; Score 2495; DB 21; Best Local Similarity 98.7%; Pred. No. 3.5e-143; Matches 464; Conservative 4; Mismatches 2;

Sednence

Length 470;

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas (I igand system, by binding to Fas on the cells with an abnormal Fas/Fas apoptosis in cells with a normal system, by indining binding between apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidiabetic, and hibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent apoptosis by binding to cell surface Fas or inhibit it by competitive compactives apoptosis. Hashimoto disasse, permitticious or hypoplastic versus host disease, sloreoderma, permitcious or hypoplastic community Addison's disease, scleroderma, goodpasture syndrome, Cohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, allergy, arteriosclerosis, myocarditis, cardiomyopathy glomerulonephitis, hepatitis (fulminant, chronic, viral (E, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of the native ligand, do not induce liver disease, and have reduced risk of which is described in the method of the invention. Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection. New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems Takahashi Tamaki I, Nakahara K, Claim 2; Page 169-170; 263pp; English. 98JP-0276882. 99EP-0307711. 98JP-0276881. Haruyama H, (SANY ) SANKYO CO LTD. WPI; 2000-258930/23. N-PSDB; AAA11644. 29-SEP-1999; 05-APR-2000. 30-SEP-1998; 30-SEP-1998; Serizawa N, EP990663-A2 Synthetic. 

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                                                                                                                                             YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                  121 ysnnwyfdvwgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvs 180
                                                                                                                                                                     YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                       KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                  WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
       MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                          apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                      myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                    HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                  Anti-Fas humanised antibody HFE7A heavy chain.
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20..470
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/label- CDR_H2
/note= "claim 9"
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label= Variable
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This is the amino acid sequence of the VD type humanised heavy
chain of murine anti-human Fas monoclonal antibody HFE7A.

Edision of murine anti-human Fas monoclonal antibody HFE7A.

E coli
pgHSL7A62 carrying a fusion

E ragment of the humanised VD type HFE7A heavy chain and DNA
encoding human IgG1 constant region (see AAV70079), and is deposited
as FERM BP-6074 (Claimed). The invention provides methods for

E producing humanised antibodies by culturing host cells. Humanised
versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
of inducing apoptosis in abnormal cells expressing Fas, and of
antibodies are used to evaluate, in animal models, treatments of
antibodies are used to evaluate, in animal models, treatments of
antibodies are used to evaluate, in animal models, treatments of
alseases that involve Fas/Fas ligand interactions, and also to
treat such diseases, including autoimmune disease (e.g. systemic
lupus erythematosus, Hashimoto's disease, graft versus host disease,
Sjogren syndrome, Derniclous anaemia, Addison's disease, selenoderma,
Goodpasture syndrome, Crohn's disease, thromatoid arthritis,
autoimmune haemolytic anaemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thromatopenia purpura and
insulin-dependent diabeters), allengies, arteriosclerosis,
myocarditis, cardiomyopathy, glomecular nephritis, hypoplastic
myocarditis, cardiomyopathy, glomecular rejection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate druys in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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1 S, Shin Y, Tohru
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118..129
/label= CDR_H3
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98.5%;
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97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
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   KSCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                             YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                  361 KAKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420
                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                           LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
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Chimeric - Homo sapiens
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N-PSDB; AAA72159.
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360
                                             Gaps
                                                                                       9
                                                                                                                antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                                                                                                              GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                     YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                          181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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  Length 470;
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  Score 2485; DB 21;
Pred. No. 1.4e-142;
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                                           Mismatches
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98.78;
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                                           Conservative
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                      Similarity
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                                           463;
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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

421 421

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Intias Infortion describes a flower numerized anti-Fas antibody-Inke molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents cappetosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunodulatory, dermacological, immunosuppressive, thyromimetic, antidiabetic, antidiffertility, neuroprotective, antiviral, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's Syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, alleryy arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, Cor D) or alcoholic), and transplant rejection. (I) selectively cinhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce litver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents the much as human anti-murine antibody response. This sequence represents and human anti-marine antibody response. This sequence represents the method described in the inventy designed heavy chain which is the security of the induce lity the disease.
                                                                                                                                                        J.e.c
                                                                                                                                                              preventing
                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively
                                                                                                                                                                                                                                                                                                                      This invention describes a novel humanized anti-Fas antibody-like
                            Takahashi T;
                                                                                                                                                                                                                                                              Example reference 15; Page 134-136; 263pp; English.
                            Tamaki I,
                                                                                                                                                                                                                cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the method described in the invention.
                            Nakahara K,
                         H
                            Нагиуаша
                                                                         WPI; 2000-258930/23
                                                                                                        N-PSDB; AAA11597
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                            Serizawa
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21; Score 2485; DB 21; Pred. No. 1.4e-142; 98.7%; 98.5%; Similarity 470 AA; Seguence Query Match

ö 240 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120 Gaps 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP ó Length 470; Indels Mismatches 463; Conservative Best Local Matches 61 121 121 181 181 241 241 301 361 301 g а g òγ δ 셤 ò g οy ò g ò

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181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240

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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                        Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                 Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
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Pred. No. 5.1e-135;
9; Mismatches 8;
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                       AA.
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93.6%; Pre
tive 19;
                       AAM52156 standard; Protein; 731
                                                                                                                                                                                                                                                    26-MAR-2001; 2001WO-GB01324.
                                                                                                                                                                                                                                                                            03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
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                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                   LTD.
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                                                                                                                                                               sapiens.
                                                                         05-FEB-2002
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Best Local Simmatches 440;
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                                                  AAM52156;
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WPI; 2001-662969/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                   361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                                                                        238 kscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297
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                                                                                                                                                                                                                                                                                    LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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93.6%; Pred. No. 5.1e-135;
ive 19; Mismatches 8;
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02-OCT-2000; 2000US-237159P
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Synthetic.
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Indels

Conservative

Similarity

Best Loca Matches

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Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                                                                                                                        241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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2000US-237159P
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Homo sapiens
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                                            comprising
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Matches 439;
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having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AMM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
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                                                                            DB 22;
                                                                           93.7%; Score 2358.5; DB 93.6%; Pred. No. 1e-134; iive 19; Mismatches
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2000US-237159P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                             Conservative
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02-OCT-2000;
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2001-662969/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
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93.6%; Pred. No. 2.3e-134;
Live 19; Mismatches 8; Indels
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                                                                                             2000GB-0008049,
2000US-237159P.
                                                                      26-MAR-2001; 2001WO-GB01324
                                                                                                                                  LTD.
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Best Local Similarity 93.6
Matches 438; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         730 AA;
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LENGTH: 476 amino acids
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                                                                                                                                                                                                       1 MGWSCIILFLVATATGVHSQ.......MHEALHNHYTQKSLSLSPGK 470
                                                                                                            Search time 82.88 Seconds
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1: /cgn2_6/ptodatu2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatu2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatu2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodatu2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodatu2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodatu2/iaa/PcTUS_COMB.pep:*
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Compugen Ltd.
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US-09-028-516-13

US-09-028-985-71

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US-09-028-985-71

US-09-028-7378-67

US-09-485-7378-67

US-08-733-450-8

US-08-733-450-8

US-08-733-450-8

US-08-733-450-8

US-08-887-3528-14

US-08-887-3528-14

US-09-109-207C-14

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18

US-09-206-005-16

US-09-206-005-16

US-09-206-005-16

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US-09-205-205-208-207C-18
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US-08-466-163B-8
US-09-679-397-2
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                GenCore version (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
                                                                                                           August 14, 2002, 15:17:08
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum |
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; Pred. No. 5.9e-163;
19; Mismatches 27;
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                       ERNST & KURZ
N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CIASIPECATION: 435
CIASIPECATION: 435
PRIOR APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTOCNEY AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                       STREE: BOTHWELL, FIGG, E. STREE: 555 THIRTEENTH ST. N. CITY: WASHINGTON STATE: D. C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity 89.1%;
Matches 424; Conservative 19
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MOLECULE TYPE:
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1 MDWTWRFLFVVAAATGVQSQMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYALSWVRQAP 60
                                                                                                                                                                                                                                                                                                  355 IEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNY
                             61 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNR-
                                                                                                                                                      EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION
APPLICANT: Co. Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: William M. Smith STREET: One Market Plaza, Steuart Tower, CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11823-37-3
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TELEPHONE: 415-326-2400
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 449 amino acids TYPE: amino acid
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80 NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139
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Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Genzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Antibody Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
  Length 449;
                                          Indels
88.6%; Score 2230; DB 1;
93.1%; Pred. No. 2.2e-162;
iive 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDeatin (Genentech)
CNRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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20-Feb-1998
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APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
FRICK APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                            Matches 420; Conservative
  Query Match
Best Local Similarity
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ZIP: 94080
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                            Matches 408; Conservative
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APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                              Similarity
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APPLICANT: Hillman
                                                                                                                                                                                                                                                                                   US-09-026-985-71
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/09026985

Patent No. 6133426

GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.

APPLICANT: Deong, Steven R.

APPLICANT: Deong, Steven R.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

CONPERT USA

COMPTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                         Length 452;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                    87.8%; Score 2210.5; DB 3; 90.3%; Pred. No. 6.9e-161; ive 27; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 650/255-5530
TELEFRAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 antino acids
TYPE: Amino Acid
FILING DATE: 21-Feb-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 Matches 408; Conservative
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                            TOPOLOGY: Linear
                                                                                                                                                                                          US-09-027-449-71
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Best Local S
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121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 2210.5; DB 4
90.3%; Pred. No. 6.9e-161;
ive 27; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P1085R3-1
APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/09049672A; Patent No. 6135941
                                                              ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34.659
REFRENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEFRAX: 650/252-5530
TELEFRAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IM
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424 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                               Sequence 67, Application US/09485737B Patent No. 6350860
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                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: SYNTHETIC
                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-09-485-737B-90
                                                                   US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-485-737B-67
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pate
SEQ ID NO 67
LENGTH: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 ISCVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 2207.5; DB 4; Pred. No. 1.2e-160; 20; Mismatches 27;
                                                                                                                                              OPERATING SYSTEM: DOS SOFTWARE: FASTSEM DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                          3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                         PF-0497
                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.78;
89.28;
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8:
                                                                                                                         E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGSY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 89.2
Matches 414; Conservative
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
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Best Local Similarity
                                                      Palo Alto
                                                                                  USA
                          ADDRESSEE:
                                                                                                                                          COMPUTER:
                                                                  STATE: C
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APPLICANT: BUYSE, Marie-Ange
APPLICANT: BUYSE, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 YEDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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121 YSNNW----YFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 175 | STATEMENT | STATEMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.2%; Score 2146; DB 4; Length 4
85.3%; Pred. No. 6e-156;
Live 25; Mismatches 37; Indels
                                                                                                             ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 03-08/793,450 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660-118-0 PCT
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 660
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85,29
Best Local Similarity 85,39
Matches 405; Conservative
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                        22202
                                                                                                                                                                                                                              COUNTRY:
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                                   APPLICANT: BUYSE, MATIE-ANGE
APPLICANT: BUYSE, MATIE-ANGE
APPLICANT: BUYSE, MATIE-ANGE
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERPERSON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
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APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZENEK, MICHEL
APPLICANT: CHABINEK, MICHEL
APPLICANT: CHABINEK, MONOCLONAL RECOMBINANT ANTI-RHESUS
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS
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88.0%; Pred. No. 1.1e-157;
1ve 20; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-793-450-8; Sequence 8, Application US/08793450; Patent No. 6312690; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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Matches 409; Conservative
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LENGTH: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                 421 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
ATTORNEY AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
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INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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Amino Acid
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1.55 inch, 1.44 Mb floppy disk
SOFTWHEN THE COMPUTER: 1.50 inch 1.
                                                                                                               Sequence 22, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Peul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genettech, Inc.
STREET: 1 DNA Way
CITT: South San Francisco
STATE: California
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88.3%; Pred. No. 1.1e-155;
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0705
TELECOMMUNICATION INFORMATION:
TELEPAN: 650/252-1994
TELEFAX: 650/252-1994
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 454 amino acids
Amino Acid
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Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
                                                                                          US-07-934-373C-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
                                                                                                                                                                                                                                                                LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 240
                                                                                                                                                                                                                                                                                                                                                                                                                           LIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
                                                                                                                                                                                               NQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
                                                                                                                                                                                                                                                                                                                                    LOSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 256
                                                                                                                          20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
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                                                       DB 5; Length 454;
                                                                                        Indels
                                                      Query Match 85.1%; Score 2142.5; DB 5; Best Local Similarity 88.3%; Pred. No. 1.1e-155; Matches 401; Conservative 20; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSE: Genenteck STREET: 1 DNA WAY
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Generated, Inc.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generated, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                     437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 709P2PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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FEELEX: 910/371-7168
INFORMATION FOR SO ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
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amino acid
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TOPOLOGY:
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TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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Patent No. 5994511
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                 240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 YNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTV 138
                                                                                                                                                                                                                                                                                                                            SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                              SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSR 378
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                                                                                                                      Length 451;
                                                                                                                                                        Indels
                                                                                                                    85.0%; Score 2141; DB 2;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
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APPLICATION NUMBER: US/08/887,3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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03-Jul-1997
N: 530
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                               ; TOPOLOGY: Linear
US-08-887-3528-14
                                                                                                                                    Best Local Similarity
Matches 399; Conserv
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US-08-887-352B-16
                                                                                                                      Query Match
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240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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                                                                                                                                                         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                180 SSGLYSLYSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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                                                                     Length 451;
                                                                                                             Indels
                                                              85.0%; Score 2141; DB 2;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: INA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 65, Application US/08466151 Patent No. 6037453
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                                                                 Query Match 85.0%
Best Local Similarity 88.3%
Matches 399; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94080
US-08-887-352B-16
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us/09/109,207C

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FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
LENGTH: 451
                                                                                                                                                                         NAME/KEY: Artificial LOCATION: 1-451
                                                                                                                                           ORGANISM: Artificial
                                                                                                                              TYPE: PRT
                                                                                                                                                            FEATURE:
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Improved Anti-IgE Antibodies and Method of Improving Polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.0%; Score 2141; DB 3;
88.3%; Pred. No. 1.4e-155;
ive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                     P0718P2C1D1
                                                                                                                                                FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craiq G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-109-207C-14

Sequence 14, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
TITLE OF INVENTION: Improved Anti-IC
                                                                                          APPLICATION NUMBER: 08/185899
FILING DATE: 25-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
                                                                                                                                                                                                                                  NAME: Svoboda, Craig G.
REGIZTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/25-1489
INFORMATION FOR SEG ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                               JMBER: 08/405617
15-MAR-1995
              APPLICATION NUMBER: 08/40 FILING DATE: 06-Jun-1995 APPLICATION NUMBER: 08/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 399; Conservative
                                                            FILING DATE: 15-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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1410 GGPSVFLFPPRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                   79 YNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTV 138
                                                                                                                                         Gaps
                                                                                                                                                                                  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVRQAPGQGLEWMGEIDPSDSYTN 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                         ;
CTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-14
                                                                                                                                         Indels
                                                                                               85.0%; Score 2141; DB 4;
88.3%; Pred. No. 1.4e-155;
iive 23; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 14, 2002, 15:17:09
Job time: 692 sec
                                                                                               Query Match
Best Local Similarity 88.39
Matches 399; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:19:02 ; Search time 108.64 Seconds (without alignments) 415.703 Million cell updates/sec

US-09-499-662-157 2518 1 MGWSCIILFLVATATGVHSQ........MHEALHNHYTOKSLSLSPGK 470 Title: Perfect score: Sequence:

Scoring table:

283138 seqs, 96089334 residues BLOSUM62DX Gapop 10.0 , Gapext 0.5 Searched:

283138

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_71:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	qamma		qamma	gamma-2	Ig gamma-4 chain C	Ig gamma-2a chain	Ig gamma-2b chain		Ig heavy chain pre	gamma-	Ig gamma-1 chain -	Ig heavy chain V r	C	Ig gamma 2a chain	Ig gamma 2b chain	Ig gamma-1 chain C	gamma c	Ig gamma 1 chain c		Ig gamma 3 chain c	Ig gamma-2 chain C	Ig heavy chain C r		Ig gamma-1 chain C			gamma-2b		
SUMMARIES	ΩI	Синп	A23511	A60764	G2HU	G4HU	S37483	G2MS11	S40295	S22080	S01321	S31459	869339	PC4436	147159	147160	S31866	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	G3MSC	G1MS	PS0018	G1MSM	G3MSM
	DB	П	7	7	-	٦	7	-	7	7	7	7	7	~	7	ď	4	7	7	Н	~	-	7	-1	~	-	Н	~	<b>–</b>	П
	Query Match Length	330	377	377	326	327	469	474	446	470	475	472	374	444	328	328	255	234	328	323	328	329	308	289	326	329	324	333	393	398
or (	Query Match	8.69	65.1	S	63.9	e,	8		9.09	٠		58.8	٠	57.2	50.3	50.1		49.4	49.0	•	48.9	48.1		45.9		45.7	45.5	45.5	45.3	45.2
	Score	1758	٠	۲.	_	1599.5	1591.5	1535	1525	_	1482.5	1481	1443	1440.5	1267	1261	1253	1245	1235	1231.5	1231	1210.5	1165.5	1157	1155	1150	1145	1144.5	1140	1139
	Kesult No.	Т	7	Э	4	S	9	7	æ	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A. Contents: Eu A. Accession: A90564
A. Molecule type: protein
A. Note: this sequence the Glm(non-1) markers, 239-Glu and 241-Met
A. Note: this sequence the Glm(non-1) markers, 239-Glu and 241-Met
B. Ponsting1, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A. Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
G2MSA	S0084/	G2MSAB	GZMSAM	PS0019	S06611	G2MSBM	147162	538864	S14683	S04845	S69131	S38950	A49444	S69340	B46529
0	7	-1	-	~	~	Н	~	~	~	7	7	~	~	~	7
330	329	332	399	322	327	405	277	548	627	549	241	246	220	249	572
44.8	44.8	44.7	44.6	44.3	43.4	42.9	42.5	40.1	37.8	36.8	34.7	33.0	31.7	30.8	30.8
1129	1127.5	1126.5	1124	1115	1093.5	1080	1070	1010	951	925.5	872.5	832	797	776.5	776.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A.Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A; Reference number: A93433; MUID:82274238
A;Accession: A93433
A; Molecule type: DNA
A; Residues: 1-330 <ell></ell>
A;Cross-references: EMBL:Z17370
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
A; Note: Lys-330 is removed after translation
R; Harris, L.J.
submitted to the EMBL Data Library, October 1992
A; Reference number: S33904
A; Accession: S36861
A; Molecule type: DNA
A; Residues: 2-330 <har></har>
A; Cross-references: EMBL: 217370
R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A, Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference number: S33887; MUID:83001943
A; Accession: S33887
A; Molecule type: DNA
A; Residues: 88-113; 235-330 <tak></tak>
A; Cross-references: EMBL: Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A; Reference number: A90563; MUID:71064024
A;Contents: myeloma protein Eu
A; Accession: B90563
A; Molecule type: protein
A; Residues: 1-96,'R', 98-135 <cun></cun>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R; Rutishauser, Ü.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A, Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A; Reference number: A90564; MUID: 71064025
A. Contents: E.

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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A;Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u) with an IGHG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                      Til gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Homo sapiens (man)
C.baces and Hay-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.bacession: A60764
R.Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A.;Title: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB:1GHG3
A; Cross-references: GDB:119339; OMIM:147120
A; Cross-references: 14432.33
A; Map position: 14432.33-14432.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;MoLecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.1%; Score 1639.5; DB 82.8%; Pred. No. 9.9e-87; iive 7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               form LAT - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 82.8
Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-3 chain C region,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A.Gross-references: GDB:120085; OMIM:147100
A.Gross-references: 99/1; 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and igav, the subunits associate into la C.Superfamily: immunoglobulin C region; immunoglobulin homology cimix
C.Superfamily: immunoglobulin homology cimix
F:130-206/Domain: immunoglobulin homology cimix
F:243-310/Domain: immunoglobulin homology cimix
F:243-310/Domain: immunoglobulin homology cimix
F:243-310/Domain: immunoglobulin homology cimix
F:243-310/Domain: immunoglobulin homology cimix
F:210-370:sulfide bonds: interchain (to light chain) #status experimental
F:103/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                         A.Accession: M91733
A.Molecule type: protein
B.Ochec: this sequence has the Glm(3) and Glm(non-1) markers
B.Gall, W.E.; Edelman, G.M.
B.Achenistry 9, 3188-3196, 1970
A.Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A.Roference number: A90565; MUD:71064027
A.Contents: annotation; disulfide bonds
A.Roference number: A90565; MUD:71064027
A.Contents: annotation: disulfide bonds
A.Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A.Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A.Reference number: A91667; MUD:77070267
A.Contents: annotation; disulfide bonds
C.Genetics:
                                                                                                               ,27
                                                                                                                                                                                                                       KOI
                                                                               A Molecule type: protein
A;Residues: 1-34, 0', 36-96, K', 98-115, 0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A;Residues: 1-34, 0', 36-96, K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W'; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl K
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl K
A;Contents: myeloma protein KOL; disulfide bonds
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Pred. No. 1.5e-93;
3; Mismatches 0;
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A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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99.1%;
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Best Local Similarity 99.1
Matches 327; Conservative
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Amap position: 14932.33-14932.33
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C; Complex: An immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-87/Domain: immunoglobulin homology < IM2>
F; 20-87/Domain: immunoglobulin homology < IM3>
F; 213-202/Domain: immunoglobulin homology < IM3>
F; 14/Pisulfide bonds: interchain (to light chain) #status experimental
F; 102.103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 102.103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 102.103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 102.103,106,109/Disulfide bonds: interchain (to heavy chain) #status predicted
                                                                                                                                                                                                                residues 25, 59, 60, and 264-268 that shown in having 60-Ala and in the ami
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C;Species: Homo sapiens (man)
C;Date: 07-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
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                                                                                                                                                                                                                                                                                                 Rimilstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
Aritle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Contents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUID:69064124
A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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91.8%; Pred. No. 4.1e-85;
tive 10; Mismatches 13;
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A;Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                                                      A;Contents: annotation; Zie, revisions to A;Note: the revised sequence differs from
  number: A93132; MUID:80114419
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                                                                                                                                                                   March 1980
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Matches 303; Conservative
                                                                                                                                                                                            A; Reference number: A94591
                                                                                  A; Molecule type: protein
A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, M.
                                                      A; Accession: A93132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
  A; Reference
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A; Molecule type: DNA
A; Residues: 1-326 CELL>
A; Cross-references: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A; Mole: Lys-326 is probably removed posttranslationally
A; Cross-references: GB: V00554; GB: J00230; NID: g32759; PIDN: CAB58438.1; PID: g6066056
A; Note: Lys-326 is probably removed posttranslationally
B; Wand, A.C.; Tung, E.; Pudebberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fA; Reference number: A92809; MUID: 81007873
A; Rocession: A92809
A; Molecule type: protein Til
A; Accession: A92809
A; Molecule type: protein
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.: Hofmann, T.
Can. J. Biochem: 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Accession: A0787
A; A; Contents: Molecule tile
A; Reference number: A90752; MID: 80001357
A; A; Accession: A0787
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A; Molecule type: protein
A; Molecule type: protein
A; Notes: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-A; Note: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ', 175, 'B', '177-193, 'D', 195-196, 'Q', 198-A; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Reference number: A93906; MUID:82197621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV------ 238
                                                                                                                                                                                                                                                                                                                                                          273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPFCPRCPAPELLGGPSVFLFPPKPKDT 180
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                                                                                                                                                                                                                   141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALFSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                            Length
                                                                                                                                                                11; Indels
                                                                                                       Score 1637.5; DB 2;
Pred. No. 1.3e-86;
7; Mismatches 11;
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology
                                                                                                       65.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 82.8
Matches 312; Conservative
                                                                                                         Query Match
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A; Molecule type: mRNA
A; Residues: 1-469 <DUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 276-345/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                             Similarity
    A;Status: preliminary
                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 299;
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A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap campled bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85, Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                               constant
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                                                                                                                                                    A; Note: the sequence was determined from the germline gene R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem, J. 117, 33-47, 1970 A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the A; Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/LDomain: immunoglobulin homology <IM3>
F;140-1201, 247-305/Disulfide bonds: #status predicted
F;27-83,141-201, 247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 327;
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A;Reference number: S37483
A;Accession: S37483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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A; Residues: 1-30;81-326 <PLN>
C; Genetics: A; GBB: IGHG4
A; Gene: GDB: IGHG4
A; Cross-references: GDB: 119340; OMIM: 147130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 91.8
Matches 303; Conservative
                                                                                                            A; Molecule type: DNA
A; Residues: 1-327 <ELL>
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R; Ducancel, F.F.D.
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                                                                                         A; Accession: A90933
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Ignama-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Apecies: J-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26233; A36398
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL. Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi A;Reference number: S25057
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Ascession: S25057
Ascession: S25057
Ascession: S25057
Ascession: Parliminary
Ascession: Preliminary
Ascession: Preliminary
Ascession: 1-474 FIES
Ascession: BMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827
Ascression: Ascession: Asc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                   Indels
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Blattner, F.R.
           DB 2;
                                                                                                              Conservative 63; Mismatches 105;
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A;Residues: 138-161, 'L',163-189, 'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A)Note: Les sequence was determined from the germl:
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattl
Science 206, 1299-1303, 1979
63.2%; Score 1591.5; D
63.3%; Pred. No. 7e-84;
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C, Accession: S40293
C, Accession: S40293
R; Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.,
submitted to the EMBL Data Library, January 1993
A; Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A; Reference number: S40295
A; Accession: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin pyroglutamic acid
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;118-446/Domain: C region <CHR>
F;118-444/Domain: C region <CHR>
F;118-414/Domain: C2 region <CH2>
F;215-230/Region: hinge
F;231-340/Domain: C3 region <CH2>
F;315-340/Domain: C3 region <CH2>
F;341-446/Domain: C3 region <CH2>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;224,227,229/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain (to light chain) #status experimental
F;224,227,229/Disulfide bonds: interchain (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Mus musculus (house mouse)
C.Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
  413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPEL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                       414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                     PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
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63.3%; Pred. No. 4.2e-80;
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A Accession: A422.

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     untranslated regions of the murine gamma2b
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A;Title: Structure of the constant and 3'A;Reference number: A26235; MUID:80081501
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288; Conservative
                                                                             A; Accession: A26235
                                                       A; Contents: MPC 11
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Best Local Si
Matches 288;
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419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Best Local Similarity 59.5%
Matches 284; Conservative
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                                                                                                                                                                                                                                                                                                                           A; Accession: S01321
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                                                                                                                                                                                                       Igheavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $22080; $06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Retaus: preliminary
A;Accession: $22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 < SANN
A;Residues: 1-470 < SANN
A;Residues: 1-470 < SANN
A;Residues: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: $06610; MUID:90097956
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C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNR--D 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 FVDDVEVNTATTKPREEGFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTIS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTP 418
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3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
C; Genetics:
                                                                                       Query Match
Best Local Similarity 60.68
Matches 286; Conservative
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A;Introns: 98/1; 111/1; 221/1
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of mouse recombinant immunoglobulin directe
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Sacession: S31459
R;Patri, S; Nau, F.
Ssubmitted to the EMBL Data Library, December 1992
A;Reference number: S31459
                                                                                                                                                                                                                                                 30-Sep-1989 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 SGPTSTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-475 <DEL3.
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 WNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICUVNHKPSNTKVDKRVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                               C; Accession: S01321
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immuno A; Reference number: S01320; MUID: 88329081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 475;
58.9%; Score 1482.5; DB 2; Length
59.5%; Pred. No. 1.2e-77;
Live 69; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:1-19/Domain: signal sequence #status predicted <SIG>F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>F:159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision
                                                                                                                                                                                     gamma-2b chain precursor - mouse
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Systems (Man) V region precursor - human C; Species: Homo sapiens (Man) Systems (Man) Species: Speci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
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                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                       homology
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A; Accession: S31459
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-472 < PAIP>
A; Cross-references: EMBL: X69797
C; Superfamily: immunoglobulin C region; immunoglobulin B; 277-346/Domain: immunoglobulin l
                                                                                                                                                                                                                                                                                                                                                                                   112;
                                                                                                                                                                                                                                                                                                                       58.8%; Score 1481; DB 2; 60.0%; Pred. No. 1.5e-77; ive 66; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 60.0 ses 285; Conservative
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Best Local S:
Matches 285
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C;Species: Mus musculus (house mouse)
C;Species: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
B;Akashi, S; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harri Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a physicence number: JC5810; MUID:98063277
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                                                                                        GLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTAYMELSSLRSEDTAVYYCARN-RDY
                                                                                                                                                                                                               SNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
                                                                                                                                                                                                                                                                                   NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK
                                                                                                                                                                                                                                                                                                                                                          242 SCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 AKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
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                                                                      5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVRQAPGQ
                                                                                                                                                                            65 ALEWLALIFWDDD-KRYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGY
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Length 374;
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A; Residues: 1-444 ARANA
C; Comment: This catalytic antibody has peroxidase oxidase activi
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 231-320/Domain: immunoglobulin homology <IMM>
F; 22/Disulfide bonds: interchain (to 98) #status predicted
F; 99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1440.5; DB 2; Length
Pred. No. 2.8e-75;
3; Mismatches 93; Indels
Score 1443; DB 2;
Pred. No. 1.7e-75;
3; Mismatches 56;
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58.4%; Pre-
tive 78; 1
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60.3%;
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Matches 267; C
 Query Match
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Search completed: August 14, 2002, 15:19:03 Job time: 691 sec
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: 147159
A;Reference number: 147159
A;Accession: 147159
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                        230
                                                                                                     VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124 C; Genetics: A;Genetics: A;Genetics: A;Genetics: C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 433
                                                                                                                                                                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
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               G; Species: Sus scrofts domestic and projection of Species: Sus scrofts domestic and (c) because in 1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000 C; Accession: 147160
B; Kacskovics, I:, Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the CDNA sequence A; Reference number: 147158; MUID:95015845
A; Accession: I47160
A; Accession: I47160
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 «KAC>
A; Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C; Genetics:
A; Gene: IgG2b
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology < IMM>
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gamma 2b chain constant region - pig (fragment)
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2002, 15:23:16; Search time 53.64 Seconds (without alignments) 339.265 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-499-662-157 2518 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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Eukarvota; M	etazoa; Chordata		a: Vertebrata; Euteleos
Mammalia; Eu	Mammalia; Eutheria; Primates;		Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	906;		
[1]			
SEQUENCE FROM N.A.	K N.A.		
MEDLINE=8227	MEDLINE=82274238; PubMed=6287432;	7432;	
Ellison J.W.	, Berson B.J., H	ood L.E.;	
"The nucleot	ide sequence of	a human i	"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acid	Nucleic Acids Res. 10:4071-4079(1982).	079(1982)	•
[3]			
SEQUENCE OF	1-135 (MYELOMA P.	ROTEIN EU	٠.
MEDLINE=7106	4024; PubMed=548	9771;	
Cunningham B	.A., Rutishauser	U., Gall	W.E., Gottlieb P.D.,
Waxdal M.J.,	Edelman G.M.;		Waxdal M.J., Edelman G.M.;
"The covalen	t structure of a	human ga	umma G-immunoglobulin. V
acid sequenc	e of heavy-chain	cyanogen	bromide iragments Hl-H
Blochemistry	/6T)0/TE-TQTE:6	. (0	
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"The covalen	"The covalent structure of a	himan da	mma G-immunoalobulin. 8
acid segmence	e of heavy-chain	Cvanogen	of heavy-chain cyanogen bromide fragments H5-H7
Biochemistry	9:3171-3181(197		1
[4]			
SEQUENCE (MY	ELOMA PROTEIN NI	豆).	
MEDLINE=7707	0269; PubMed=826	475;	
Ponstingl H.	Ponstingl H., Hilschmann N.;		
"The rule of	antibody struct	ure. The	"The rule of antibody structure. The primary structure of a
monoclonal I	gG1 immunoglobul	in (myelo	ma protein Nie). III. The
chymotryptic	peptides of the	H-chain,	alignment of the tryptic
peptides and	discussion of t	he comple	peptides and discussion of the complete structure.";
Hoppe-Seyler	s Z. Physiol. C	hem. 357:	1571-1604(1976).
[5]			
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MEDLINE#6320	TIST; FUDMEN=060	4734;	
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Hoppe-seyler	s z. Pnysioi. C	nem. 364:	/13-/4/(1983).
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MEDLINE=7106	MEDLINE=71064027; PubMed=4923144;	3144;	
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1	W.E., Edelman G.M.;		

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                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                            Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal igdl immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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K -> R (IN GIM(3) MARKER).
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D -> E (IN GIM(NON-1) MARKER).
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L -> M (IN GIM(NON-1) MARKER).
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                                MEDLINE-77070267; PubMed-1002129;
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SWART; SM00407; IG_Like; 1.
PROSITE; PS00290; IG_MHC; 2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-80114419; PubMed=118920;
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                                                                                                                             MEDLINE-83001943; PubMed-6811139;
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MEDLINE=84235992; PubMed=6329676;
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 NCBI_TaxID=9606;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S -> A (IN MYELOMA PROTEINS TIL & ZIE).
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SMART: SM00410; 1G_1lke; 1.
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Immunoglobulin domain; Immunoglobulin C region.
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                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                 MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Human immunoglobulin subclasses. Partial amino acid sequence of constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                             Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35940 MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1e-103;
  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 1599.5; 91.8%; Pred. No. 1e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                            EMBL; K01316; AAB59394.1; ALT_INIT.
                                                                               SEQUENCE FROM N.A.
MEDLINE-83157104; PubMed-6299662;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                         SEQUENCE OF 1-30 AND 81-326
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3. SMART; SMO0410; IG_like; 1. SMART; SMO0407; IGC1; 2.
OCT-2001 (Rel. 40, Last gamma-4 chain Cregion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 303; Conservative
                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                              HSSP; P01842; 7FAB.
MIM; 147130; -.
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327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                       A02150; G4HU
                                                           NCBI_TaxID=9606;
16-OCT-2001
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Blochem. J. 151:337-349(1975).
178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                          238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297
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                                                                      381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 AA.
                                                                                                                                                                                                                        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
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Pratt D.M., Mole L.E.;
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MEDLINE=70110015; PubMed=5461106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma chain C region.
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SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                                                                                                                                     Biochemistry 13:4804-4811(1974).
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InterPro: IPR003006; Ig_MHC.

InterPro: IPR003509; Ig_C1.

InterPro: IPR003600; Ig_like.

Pfam: PF00047; ig; 3.

SMART: SMO04010; IG_like; 1.

SMART: SMO0407; IGC1: 2.

PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                         Biochemistry 10:9-17(1971).
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79
105
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202
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308
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329 AA;
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SEQUENCE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                        RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 383
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 263
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentía; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                          DB 1; Length 323;
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                                                          M (IN D11 MARKER).

A (IN E15 MARKER).

E (IN REF. 2).

VPV (IN REF. 2).

E (IN REF. 5).

E (IN REF. 5).

E (IN REF. 5).

E (IN REF. 5).

C (IN REF. 5).

Q (IN REF. 5).

Q (IN REF. 5).

Q (IN REF. 5).

G (IN REF. 5).

D (IN REF. 5).

M (IN REF. 5).
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N -> E (IN REF. 2).

-> V (IN REF. 2).

-> D (IN REF. 3).

N -> D (IN REF. 5).

E -> Q (IN REF. 5).

E -> Q (IN REF. 5).

M -> D (IN REF. 5).

E -> Q (IN REF. 5).

N -> D (IN REF. 5).

G9E8AA118D579A8B CRC64;
         Pfam; PF00047; 1g; 3. SMART; SM000407; 1g; 3. TGG1; 2. TGG1; 2. TGG1; 3. TGG1; 3. TGG1; 1. TEMUNOG10bulin Gomain; Immunoglobulin Gomain; Immunoglobulin C region.
                                                                                                                                                                                                                                                        48.9%; Score 1231.5; DB 70.0%; Pred. No. 2.8e-78; iive 34; Mismatches 57
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
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Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVFSCSVMHEALHNHYTQKSLSLSPGK 470
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MEDLINE=71058471; PubMed=5538606;
                                                                                 ZPOZOZOEZ
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IPR003597; Ig_c1.
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488
1173
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256
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266
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323 AA;
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173
187
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P01862;
  InterPro;
                                                  NON_TER
VARIANT
CONFLICT
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Best Local 9
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Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
-!- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
13 INBRED GUINEA PIGS.
PIR; A02151; G2GP.
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                                                                                                                                                                                                                                                                                            carboxy1-terminal
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Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 134-226.

BEDILINE-7036072; PubMed-4429665;

Tracey D.E., Cebra J.J.;

"Primary structure of the CH2 homology region from guinea pig 1962
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                                                                                                                                                                                                                                  Turner K.J., Cebra J.J.; "Structure of heavy chain from strain 13 guinea "Structure of heavy chain from strain a sequence of immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
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-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
                                         435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL MEADY CHAINS.
            318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                          Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19304-4308(1980).
                                        378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein 2UC. Structure of the Fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC)
                                                                                   469
                                                                                             296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                           290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
                                                                                  436 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                           PRT;
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REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                     SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-82247835; PubMed-6808505
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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P01860;
                                                                                                                                               GC3_HUMAN
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91.4%; Pred. No. 1.6e-73;
ive 11; Mismatches 9;
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P -> L (IN OMM).
/FTId=VAR_003891.
F -> Y (IN OMM).
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F -> Y (IN OMM).
/FTIG=VAR_003896,
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T -> A (IN OMM).
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CH2.
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
SMART; SM00410; IG_Like; 1.
SMART; SM00407; IG_Like; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                  PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
MIM; 147120; -
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                                                                     GCI_RAT STANDARD; PRT; 326 AA.
P20759;
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1999 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-1 chain C region.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                             "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
PIR; PS0017; PS0017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
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013BAB45EF49B9DA CRC64;
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INTERCHAIN (WITH A HEAVY CHAIN).
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INTERCHAIN (WITH A HEAVY CHAIN).
                          419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                             region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%; Score 1155; DB 1; Length 326; 63.4%; Pred. No. 5.5e-73; tive 52; Mismatches 60; Indels 10
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                                                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin
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HINGE.
CH2.
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                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
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InterPro: IPR003006: Ig_MHC.
InterPro: IPR003597; Ig_c1.
Pfam; PF00047; Ig; 3.
SWART; SW00407; IGc1; 2.
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176
326 AA;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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Transmembrane; Alternative splicing.
NON_TER 1 1 7 CH1.
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65.0%; Pred. No. 1.2e-72;
iive 44; Mismatches 68;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
1g gamma-3 chain C region, secreted form.
Mus musculus (Mouse)
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438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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CH2.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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Best Local Similarity 65.08
Matches 215; Conservative
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380 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
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MEDILINE-80012837, PubMed-113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDILINE-80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                SEQUENCE FROM N.A.

BEDILINE-BRO045036, Pubmed-115593;
HONJO T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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MEDLINE-73008889; PubMed=5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                         324 AA
                                                     440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                      299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
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J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE-78242288; PubMed-98524;
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EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00795; CAA24175.1; -.
PIR; A02159; GIMS.
HSSP; P01842; 7FAB.
                                                                                                                                                           STANDARD;
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Cell 18:559-568(1979).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                            Pfam; PF00047; 1g; 3. SMATT; SMO047; 1g; 1. PF051F; SMO47; 1Gcl; 2. PF051FE; PS00290; 1G_MC; 1. Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region.
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SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
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MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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324 AA;
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                                                                  domain.
       3;
   Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_cl.
InterPro; IPR0035097; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfan; SM00410; Ig_like; 1.
SMART; SM004007; IGcl; 2.
PR051TF; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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30 MAX-2000 (Rel. 39, Last annotation update)
31 gamma - 1 chain C region, membrane-bound form.
Mus musculus (Mouse).
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HSSP; P01842; 7FAB.
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ALERNATUR PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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MEDIINE-8222190; PubMed-6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
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SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197625; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
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                                                                                                                                                                                                                                                 SEQUENCE OF 323-366 FROM N.A. MEDINE-82115295; Pubmed-6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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INTERCHAIN (WITH A HEAVY CHAIN).
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4CC88343B7A1CE27 CRC64;
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62.2%; Pred. No. 7.6e-72;
tive 55; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ", 79:2623-2627(1982).
                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
PIR; B02129; GIMSH.
HSSP; P01842; 7FAB.
INTERPO: IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                              gamma chains.";
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393 AA;
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mmunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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             141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                               258
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                                                                                                                              173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYIIPPPK 232
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                                                                             201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
                                                                                                                259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                  319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1963 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
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                                                                                                                                                                                                                                                                      439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
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EMBL; V01526; CAA24767.1; ALT_SEQ. PIR; A02155; G3MSM.
INSP: PO1857; IFC1.
INTERPRO; IPR003006; Ig_MHC.
INTERPRO; IPR003597; Ig_C1.
INTERPRO; IPR003597; Ig_C1.
INTERPRO; IPR00400; Ig_like.
SAMRT; SM00410; IG_like; 1.
SWART; SM00407; IGC1; 2.
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P03987;
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MEDLINE-81198976; PubMed-6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.'s, Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                  202 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
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                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                       Length 398;
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                                                                                                                                                                                                                CF7F264B50A41B95 CRC64;
                                                                                                                                      (POTENTIAL)
                                                                                                                                                    E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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64.7%; Pred. No. 9.1e-72;
tive 44; Mismatches 68;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Iggamma-2A chain C region, A allele.
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                                                                                                                 POTENTIAL.
CYTOPLASMIC
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Alternative splicing
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398 AA;
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SEQUENCE FROM N.A.
  Transmembrane;
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Matches 213;
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P01863;
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GCAA_MOUSE
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EEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438 

379

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439 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

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             Ollo R., Auffray C., Morchamps C., Rougeon F.; "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
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                                                                                                                         MEDLINE-74175517; PubMed-4831970;
Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Blochem. 30:452-462(1972).
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63.9%; Pred. No. 3.5e-71;
ive 43; Mismatches 73; Indels
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                                                                             Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
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Immunoglobulin domain; Immunoglobulin C region.
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MEDLINE-81223894; PubMed-6787604;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                      Brueggemann M., Delmastro-Galfre, P., Waldmann H., Calabi F.; "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region CDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1908).
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66; Indels
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                                                                                                                                  01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
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51; Mismatches
                                                                                          329 AA.
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299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
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HINGE.
CH2.
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MEDLINE=88166903; Pubmed-3127222;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                                                                                   01-FEB-1991 (Rel. 17, Created)
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PROSITE; PS00290; IG_MHC; 1.
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DOMAIN 1 97
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P01857; TEC.
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143
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329 AA;
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HSSP; P0185
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                                            176
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                                                                                       378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437
                                                                                                                                                    MEDLINE-82037777; PubMed-6794027;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of igla and iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                         QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6;
MEDLINE-82037861; PubMed-6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreier P.H., Bothwell A.L.M. the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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21-UUL-1986 (Rel. 01, Last sequence u
15-UUL-1999 (Rel. 38, Last annotation
IIG gamma-2A chain C region, B allele.
Mus musculus (Mouse).
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PIR; A02153; G2MSAB.
HSSP; P01857; 1FC1.
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SMART; SM00410; IG_like; 1.
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P01864;
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Score 1126.5; DB 1; Length 335; Pred. No. 5.3e-71;

44.7%; 61.6%;

Query Match Best Local Similarity

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                                         141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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Gaps
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70;
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Mismatches
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us-09-499-662-157.rsp

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musculu sapien

	GenCore version 4.5			30.4 5
Copy	Copyright (c) 1993 - 2000 Compugen Ltd.		19 754.5 20 753	30.0
OM protein - protein s	- protein search, using sw model		7	29.7
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## ALIGNMENTS

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5: SP_INVertebrate:*  6: sp_mammal:*  7: sp_mhc:*  8: sp_organelle:*  9: sp_plage:*  10: sp_plage:*  11: sp_rodent:*  13: sp_vertebrate:*  14: sp_unclassified:*  15: sp_vertebrate:*  16: sp_barteriap:*  17: sp_archeap:*  18: sp_archeap:*  19: sp_archeap:*  10: sp_barteriap:*  11: sp_rodent:*  15: sp_archeap:*  16: sp_barteriap:*  17: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  17: sp_archeap:*  17: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  10: sp_barteriap:*  10: sp_barteriap:*  10: sp_barteriap:*  10: sp_archeap:*										y chance to have a	distribution.					DESCIPLIANT OF THE PROPERTY OF	4		Q99125 mus musculu	099131 mus musculu	Qyrid4 mus musculu	O95m34 equus cabal	Q96pq8 homo sapien	Q921k1 mus musculu	homo	3 mus		Object nome sapten	O96dkO homo sapien	Q91wrl mus musculu		
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InterPro; IPR003006; Ig_MHC.
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120 YDYDW-FAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFPEPVTLT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 K----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 WNSGSLSSGVHTFPALLQ-SGLYILSSSVIVISNIWPSQIIICNVAHPASSTKVDKKIEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 IEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                            tch 64.5%; Score 1623.5; DB 11; Length 473; al Similarity 62.8%; Pred. No. 1e-128; 299; Conservative 73; Mismatches 95; Indels 9;
                 InterPro; 1PR003599; Ig.
InterPro; 1PR003599; Ig.
InterPro; 1PR003597; Ig.cl.
InterPro; 1PR003006; Ig.like.
InterPro; 1PR003066; Ig.MHC.
InterPro; 1PR003596; Ig.V.
Pfam; PR00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGc!, 3.
SMART; SM00410; IGcl; 3.
SMART; SM00410; IG_like; 1.
SMART; PS00299; IG_MHC; UNKNOWN_1.
PROSITE; PS00299; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC003435; AAH03435.1; -.
HSSP; P01842; TRAB.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099LC4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                     DB 11; Length 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Strausberg R.; | Strausberg R.; | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. | EMBL | BC003888; AAH03888.1; -.. | AHSZP: PO1842; FTAB. | AHSZP: PO1842; FTAB. | AHSZP: PO1842; FTAB. | AHSZP: PR003599; Ig. | AHSZP: PR003506; Ig. | Ike. | AHSZP: PR003606; Ig. | Ike. | AHSZP: PR003596; Ig. | AHSZP: PR0047; Ig. | AHSZP: PR0047; Ig. | AHSZP: PR00409; IG; 2.
                                                                                                                                                                                                                                                                                                 90; Indels
InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 3.

SMART; SM00409; IGc1, 2.

SMART; SM00407; IGc1, 2.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 1.

PROSITE; PS00290; IG_like; 1.

SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                64.0%; Score 1612.5; DB 1.
62.7%; Pred. No. 8.2e-128;
iive 75; Mismatches 90;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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51661 MW;
                                                                                                          Matches 294; Conservative
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437 AA;
  468 AA;
                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                Ouery Match 62.5%; Score 1572.5; DB 11; Length 473; Best Local Similarity 62.5%; Pred. No. 2e-124; Matches 297; Conservative 64; Mismatches 107; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878 AAH03878.1; --
HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_WHC.
SMART; SM00407; IGC1; 3.
SMART; SW00406; IGV; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
MUS MUSCUlus (Mouse)
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SMART; SM00409; IG; 2.
SMART; SM00400; IGc1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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[1]
SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrv).",
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
HSSP: P01842; FAB.
InterPro; IPR003606; Ig_like.
InterPro; IPR003066; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
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                                                                                                                                                                                                                                                          61 GOGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                 Gaps
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                                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                 9
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                                                                     Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 PVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                                                                                 Indels
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96352328B3332ADB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
                                                                  61.6%; Score 1550; DB 11;
62.3%; Pred. No. 1.6e-122;
iive 63; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                     81 QKFKGRVTIITRDISISIAYMELSSLRSEDIAVYYCARNRDYSNNWYFDVWGEGILVTVSS 140
                                                                                                                                                                                                                                                                                                                 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                                                    318
                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                                                                                                     379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                   405
                                                                 21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNYN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 MGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 --FDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSVEIFPPREKDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                                                                                                                                                                                                                                                                                                                                                     GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEW
     Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 57.0%; Score 1434.5; DB 11; Length 473; 11 Similarity 57.5%; Pred. No. 9.1e-113; 272; Conservative 73; Mismatches 113; Indels 15;
                            95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010327; AAH10327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nl protein.
473 Aa; 51946 MW; CF625F008932AF12 CRC64;
  Score 1446.5; DB 11;
Pred. No. 7.9e-114;
); Mismatches 95; Ir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091205 PRELIMINARY; PRT; 473 AA. 091205; 10-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 51.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                          RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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59.7%; Pred
tive 70;
                              Conservative
               Similarity
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                           Matches 270;
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 Query Match
Best Local
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ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCD 244
                                                                                                       298 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
MEDLINE-98383416; PubMed-9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant regic genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP-----KSCDKTHTCPPCPA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
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            358 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 337;
                                                                                                                                                                                                                 418 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Equus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.2%; Score 1263.5; DB 6; 68.9%; Pred. No. 1.5e-98; Live 44; Mismatches 52;
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Best Local Simi
Matches 233;
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Q95M34;
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01-DEC-2001
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                                               Matches 182;
    Query Match
Best Local &
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PPSREEMTKNQVSLICLVKGFYPSDIAVEWESNGOP--ENNYKTIPPVLDSDGSFFLYSK 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISKAKGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649
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                            240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21477448; PubMed=11593034; MEDLINE=21477448; PubMed=11593034; Hu Z., Garen A.; Hu Z., Garen A.; Targeting tissue factor on tumor vascular endothelial cells an cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001). EMBL; AF272774; AAK58686.1; -. SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (FROTEIN FOR MGC:18977).
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Pred. No. 1.6e-97;
                                                                                                                 LIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.98;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.9
Best Local Similarity 99.1
Matches 230; Conservative
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                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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Q96PQ8;
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                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                       61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                         181 WNSCALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                 180 WNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 EKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGS 297
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                                                Gaps
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                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 614;
  Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 944.5; DB 4; Length 6 37.3%; Pred. No. 3.1e-71; Live 83; Mismatches 164; Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009851; AAH09851.1; -. SEEF536E77AA9BBB CRC64; SEOUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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38.4%; Score 967; DB 11;
65.7%; Pred. No. 1.3e-73;
ive 35; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 K-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN (PROTEIN FOR MGC:15420).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TKVDKRVEPKS--
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Matches 215; Conservative
                                                  Conservative
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                        Similarity
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Similarity
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SEQUENCE FROM N.A.
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GK 463
                     469 GK 470
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Matches 20
                                                                                                          Q9BRV0;
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 402
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          358 QDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTXD-SVTISWTRQNGEAVKTHTNISE 415
                                                                                              SHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLP 475
                                                                                  PSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLY 430
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-----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                         EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLP
                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWYVDGVEVHNAKTKPREEQYNST - - - YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
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                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 875.5; DB 11; Length 42.1%; Pred. No. 1.5e-65; ive 75; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                       431 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
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                                                                                                                                                                                                                                                                                                                           TISSUE-COLON;
Strausberg R.;
Submitted (SEP-2001) to the EMBI EMBL; BC013488; AAH13488.1; -.
Hypothetical protein.
SEQUENCE 481 AA; 52022 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.18
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                         317
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                                                                                                                                                                              RESULT 11
263
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121 SYSSCQNDYYYYYMDVWGKGTTVTVSSASPISPKVFPLSLCS-TQPDGNVVIACLVQGFF 179
335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%; Score 866; DB 4; Length 500; 41.5%; Pred. No. 1e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00047; 19; 4.

SMART; SM00409; IG: 4.

SMART; SM00400; IG: 1.

SMART; SM00406; IG: 1.

SMART; SM00410; IG_like; 1.

SMART; SM00410; IG_like; 1.

Hypothetical protein:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 54.2 KDA PROTEIN.
HOMO saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PROSTATE;
Straubberg K.;
Submitted (APR-2001) to the EN
EMBL; BC005951; AAH05951.1; -
HSSP; P01789; 1MCP
InterPro; IPR003599; Ig-
InterPro; IPR003599; Ig-cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSLGT-QTYICNVNHKPSNTKVDKRV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 NCPGICSPPTTPPPPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 FNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.7%; Score 824.5; DB 11; Length
39.6%; Pred. No. 3e-61;
Live 76; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                  579
                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96DK0;
Q96DK0;
01-DEC-2001 (Tremblrel. 19,
01-DEC-2001 (Tremblrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 39.6
Matches 191; Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=COLON;
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                      Q91WT1
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                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462
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ID Q9
AC Q9
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 DYSNNWYF----DVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 PVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITESWKIKNNSDISSIRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                  FYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                           01-DEC-2001 (TERBLECT: 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HYPOTHETICAL 65.0 KDA PROTEIN.
HYPOTHETICAL 65.0 KDA PROTEIN.
EUKATYOTA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LSW----LFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 NKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPPSREEMT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 N-----CDKTHTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                              (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.8%; Score 826.5; DB 4; 33.0%; Pred. No. 2.8e-61; ive 93; Mismatches 178;
                                                                                                                                                                                                            597 AA
                                                                                                                                                                                                                                             (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PRIMARY B-CELLS FROM TONSILS,
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PCPAPELLGGPS------
                                                                                    VMHEALHNHYTQKSLSLSPGK 470
                                                                                                          Submitted (OCT-2001) to the EM
EMBL, BC015760, AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA, 65039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.0°
Matches 192; Conservative
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (OCT
                                                                                                                                                                                                                           Q96BB9;
01-DEC-2001 (
01-DEC-2001 (
                                                                                                                                                                        RESULT 13
Q96BB9
                  395
                                                                                    450
                                                                                                                      462
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TISSUB-CASTROK N.COSA;
ISHibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Ishibashi T., Kanehori K., Takiguchi S., Kusano J.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Rwakami B., Nagai K., Isogai T., Sugano S.;
NDDO human cDNA sequencing project.";
Submitted (CCT-2001) to the EMBL/GenBank/DBBJ databases.

EMBL; AKU58027; BAB71633.1;
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SEQUENCE 496 AA; 53532 MW; C72EEIEZ47C86FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YYGSGXYXLQHWGQGTLVTVSSASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 Y---SNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP-EP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VIVSWNSGALISGVHIFPAVLQSSG-LYSLSSVVIVPSSS-LGTQTYICNVNHKPSNTKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLMISRT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIAVEWESNGO--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHE 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO
ALPHA1 H,MYELOMA.
                                                                                                                                                                                                                                                                                                                                                                                                           Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 32.2%; Score 812; DB 4; L
Best Local Similarity 39.6%; Pred. No. 3.6e-60;
Matches 197; Conservative 65; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPLAFTQKTIDRLAGK
                                                                                                                                                 SEQUENCE FROM N.A.
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Search completed: August 14, 2002, 15:22:21 Job time: 689 sec

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